

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: October 2, 2001, 21:50:17 ; Search time 17695.9 Seconds
(without alignments)
16.701 Million cell updates/sec

Title: US-09-757-100B-17

Perfect score: 20

Sequence: 1 attctcgtcgtggtggaa 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 14155048 seqs, 7388405095 residues

Total number of hits satisfying chosen parameters: 4519004

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending_Patents_NA_Main:*

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3: /cgn2_6/ptodata/1/pna/US07_COMB.seq:*

4: /cgn2_6/ptodata/1/pna/US08_COMB.seq:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	20	100.0	20	1	PCT-US00-18999-17
2	20	100.0	20	17	US-09-377-310-17
3	20	100.0	20	29	US-09-757-100B-17
4	15.2	76.0	4	8	US-08-466-588-52
5	15	75.0	15	1	PCT-US00-18999-37
6	15	75.0	15	17	US-09-377-310-37
7	15	75.0	15	29	US-09-757-100B-37
8	14.8	74.0	35	15	US-09-144-428-31
9	14.8	74.0	35	16	US-09-218-913B-31
10	14.8	74.0	35	18	US-09-441-966-31
11	14.4	72.0	37	8	US-08-472-801-1314
12	14.4	72.0	37	10	US-08-668-235-1314
13	14.2	71.0	20	1	PCT-US97-06104-16
14	13.6	68.0	25	55	US-60-232-638-132115
15	13.6	68.0	25	55	US-60-234-017-326383
16	13.4	67.0	18	14	US-09-082-614-16
17	13.2	66.0	19	53	US-60-216-745-5602
18	13.2	66.0	20	13	US-08-965-620-718
19	13.2	66.0	25	26	US-09-660-220-136892
20	13.2	66.0	25	55	US-60-233-166-57027
21	13.2	66.0	25	55	US-60-233-166-384424
22	13.2	66.0	43	17	US-09-310-298-3092
23	13	65.0	25	55	US-60-233-166-260192
24	12.8	64.0	19	27	US-09-696-791-539
25	12.8	64.0	20	28	US-09-703-708-11309
26	12.8	64.0	20	28	US-09-703-708-17076
27	12.8	64.0	20	48	US-60-164-320-11309
28	12.8	64.0	20	48	US-60-164-320-17076
29	12.8	64.0	20	50	US-60-183-791-11309
30	12.8	64.0	20	50	US-60-183-791-17076
31	12.8	64.0	21	1	PCT-US97-07972-3
32	12.8	64.0	21	10	US-08-647-351A-3
33	12.8	64.0	21	15	US-09-100-649A-3
34	12.8	64.0	21	17	US-09-326-074-3
35	12.8	64.0	25	55	US-60-233-166-221240
36	12.8	64.0	25	55	US-60-234-017-9806
37	12.8	64.0	25	55	US-60-234-017-9815
38	12.8	64.0	25	55	US-60-234-017-336454
39	12.8	64.0	25	55	US-60-234-017-336457
40	12.8	64.0	25	55	US-60-234-017-336458
41	12.8	64.0	31	18	US-09-465-684-134
42	12.8	64.0	40	18	US-09-404-520-30598
43	12.6	63.0	20	1	PCT-US00-00583-43
44	12.6	63.0	25	55	US-60-233-166-70907
45	12.6	63.0	25	55	US-60-234-017-229508

ALIGNMENTS

RESULT 1
PCT-US00-18999-17
; Sequence 17, Application PC/TUS0018999
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Monia, Brett P.
; APPLICANT: Gaarde, William A.
; APPLICANT: Nero, Pamela S.
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
; FILE REFERENCE: ISPH-0476
; CURRENT APPLICATION NUMBER: PCT/US00/18999
; PRIOR FILING DATE: 2000-07-13
; PRIOR APPLICATION NUMBER: 09/377,310
; PRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
PCT-US00-18999-17

Query Match 100.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 attctcgtcgtggtgaa 20
Db 1 attctcgtcgtggtgaa 20
|||||

RESULT 2
US-09-377-310-17
; Sequence 17, Application US/09377310A
; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P.
; APPLICANT: Gaarde, William A.
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
; FILE REFERENCE: ISPH-0389
; CURRENT APPLICATION NUMBER: US/09/377,310A
; CURRENT FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
US-09-377-310-17

Query Match 100.0%; Score 20; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 attctcgtcgtggtgaa 20
Db 1 attctcgtcgtggtgaa 20
|||||

RESULT 3
US-09-757-100B-17
; Sequence 17, Application US/09757100B

; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P.
; APPLICANT: Gaarde, William A.
; APPLICANT: Nero, Pamela S.
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
; FILE REFERENCE: ISPH-0533
; CURRENT APPLICATION NUMBER: US/09/757,100B
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 09/377,310
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/US00/18999
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
US-09-757-100B-17

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Best Local Similarity 100.0%; Pred. No. 33;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 attctcgtcgtggtgaa 20
Db 1 attctcgtcgtggtgaa 20
|||||

RESULT 4
US-08-466-588-52/c
; Sequence 52, Application US/08466588
; GENERAL INFORMATION:
; APPLICANT: Sukhatme, Vikas P.
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO THE
; TITLE OF INVENTION: FUNCTIONAL DOMAINS OF DNA BINDING PROTEINS
; NUMBER OF SEQUENCES: 67
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: 321 North Clark Street, Suite 800
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60610
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/466,588
; APPLICATION NUMBER: 08/040,548
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/040,548
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coughlin, Daniel F.
; REGISTRATION NUMBER: 36,111
; REFERENCE/DOCKET NUMBER: arcd067
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 744-0090
; TELEFAX: (312) 245-4961
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

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OM nucleic - nucleic search, using sw model

Run on: October 2, 2001, 16:18:40 ; Search time 876.95 seconds
(without alignments)
14,320 Million cell updates/sec

Title: US-09-757-100B-12

Perfect score: 20

Sequence: 1 cctgacatcagtagcatctc 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 730101 seqs, 313950809 residues

Total number of hits satisfying chosen parameters: 854978

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N.Geneseq_0601.*

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- 21: /SID88/gcgdata/geneseq/geneseq/NA2000.DAT.*
- 22: /SID88/gcgdata/geneseq/geneseq/NA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	22 AAC65544	Human focal adhesi
c 2	16.4	82.0	20	21 AAC58860	Human tumour suppr
3	15	75.0	15	22 AAC65564	Human focal adhesi
c 4	14.2	71.0	21	22 AAF95492	Human gene single
c 5	13.6	68.0	39	21 AAA51849	Primer mcl-like-2f
6	13.6	68.0	40	21 AAA51848	Primer mcl-like-1r
c 7	13.6	68.0	42	13 AAO23448	Human heavy chain
c 8	13.6	68.0	42	14 AAO44160	Probe to isolate h
c 9	13.6	68.0	42	14 AAO44180	Probe specific for
c 10	13.6	68.0	42	17 AAT37238	Human antibody hea
c 11	13.6	68.0	42	17 AAT37216	Human antibody J s

c 12	13.6	68.0	42	18 AAV12514	Probe for human J
c 13	13.6	68.0	42	18 AAT70497	Human Immunoglobul
c 14	13.6	68.0	42	18 AAT73468	Human heavy chain
c 15	13.6	68.0	42	18 AAT73448	Human J-mu region
c 16	13.6	68.0	42	19 AAV38155	Probe oligo-1 for
c 17	13.6	68.0	42	19 AAV38128	Probe used to isol
c 18	13.6	68.0	42	20 AAZ21891	Probe used to isol
c 19	13.6	68.0	42	20 AAZ22071	Probe used to isol
c 20	13.6	68.0	42	20 AAX06008	US5874299 Seq ID 1
c 21	13.2	66.0	30	18 AAT58419	Apollipoprotein A g
c 22	13.2	66.0	30	20 AAV82530	Probe Aposma-1 use
c 23	13	65.0	23	19 AAV50010	Oligonucleotide SE
c 24	13	65.0	23	20 AAX18226	Primer lRAF616 for
c 25	13	65.0	23	21 AAX88383	FAR1 gene amplific
c 26	13	65.0	36	17 AAX65443	Mouse B7-1 hammerh
c 27	12.8	64.0	21	17 AAT39326	Primer EL074 to ge
c 28	12.8	64.0	21	17 AAT35891	Newcastle disease
c 29	12.8	64.0	21	17 AAT35924	Newcastle disease
c 30	12.8	64.0	21	19 AAV07013	Primer EL074 for N
c 31	12.8	64.0	21	19 AAV42526	PCR primer EL074 u
c 32	12.8	64.0	27	16 AAO76135	Human MDC PCR prim
c 33	12.8	64.0	28	22 AAA99419	PCR primer SEQ ID
c 34	12.6	63.0	27	18 AAX63148	Delta-9 desaturase
c 35	12.6	63.0	29	21 AAZ87393	Human thrombopoiet
c 36	12.4	62.0	27	18 AAX68545	Hammerhead ribozym
c 37	12.4	62.0	29	21 AAF00661	Human fit1 VEGF re
c 38	12.4	62.0	38	16 AAT53885	Rat ICAM hammerhea
c 39	12.4	62.0	50	17 AAT40112	Human Mer receptor
c 40	12.2	61.0	20	21 AAA78278	Human Ig H chain s
c 41	12.2	61.0	20	21 AAA78291	Human Ig H chain s
c 42	12.2	61.0	25	16 AAO94416	Rat farnesyl prote
c 43	12.2	61.0	27	13 AAO30098	JH probe #3 to det
c 44	12.2	61.0	28	20 AAX88103	Antifreeze protein
c 45	12.2	61.0	29	20 AAX88102	Synthetic antifree

ALIGNMENTS

RESULT 1

AAC65544

ID AAC65544 standard; DNA; 20 BP.

XX

AC AAC65544;

XX

DT 12-FEB-2001 (first entry)

XX

DE Human focal adhesion kinase antisense sequence #10.

XX

KW Human; focal adhesion kinase; FAK; signal transduction; cancer;

KW embryonic development disorder; angiogenic disorder; wound healing;

KW antisense; phosphothioate; ss.

XX

OS Homo sapiens.

XX

PN US6133031-A.

XX

PD 17-OCT-2000.

XX

PF 19-AUG-1999; 99US-0377310.

XX

PR 19-AUG-1999; 99US-0377310.

XX

PA (ISIS-) ISIS PHARM INC.

XX

PI Monia BP, Gaarde WA;

XX

DR WPI; 2001-006141/01.

XX

PT New antisense compounds for inhibiting focal adhesion kinase

PT expression, especially useful for inhibiting retinal

PT neovascularization, or for diagnosing and treating e.g. colon cancer -

XX

```
PS Claim 15; Column 23; 30pp; English.
XX
CC The present invention describes a number of phosphorothioate antisense
CC sequences to the human focal adhesion kinase (FAK) protein. This protein
CC is involved in integrin-mediated signal transduction, and is implicated
CC in cancer, particularly colon, breast and oral tumours, embryonic
CC development disorders, angiogenic disorders and wound healing. The
CC antisense sequences, including the one shown here, can be used in the
CC treatment of all of these.
XX
SQ Sequence 20 BP; 5 A; 7 C; 3 G; 5 T; 0 other;

Query Match      100.0%; Score 20; DB 22; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.35;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cctgacatcagtagcatctc 20
   |||||
DB 1 cctgacatcagtagcatctc 20

RESULT 2
AAC58860/c
ID AAC58860 standard; DNA; 20 BP.
AC
XX AAC58860;
XX
DT 25-JAN-2001 (first entry)
XX
DE Human tumour suppressor BRG1 deletion analysis PCR primer BRG1.R1.
XX
KW Human; BRG1; tumour suppressor gene; cancer; chromosome 19p13.1;
KW retinoblastoma tumour suppressor gene; RB; drug screening; gene therapy;
KW drug design; peptide therapy; animal model; PCR primer; ss.
XX
OS Homo sapiens.
XX
PI WO200056931-A1.
XX
PN 28-SEP-2000.
XX
PD 23-MAR-2000; 2000WO-US07678.
XX
PF 23-MAR-1999; 99US-0125806.
XX
PR (MYRI-) MYRIAD GENETICS INC.
XX
PA Wong AKC, Tavtigian SV, Teng DH;
XX
PI WPI; 2000-587668/55.
XX
DR Diagnosing a polymorphism associated with predisposition for cancer in
PT humans by determining whether there is a germline alteration of a BRG1
PT gene or its expression products -
XX
PS Example 2; Page 51; 215pp; English.
XX
CC The present invention is concerned with the use of the human tumour
CC suppressor gene BRG1 in cancer diagnosis and therapy. This gene is
CC comprised of several exons, shown in AAC58874-C58903, and has several
CC splice variants, given in AAC58906-C58912. The protein sequences for
CC these are shown in AAB27552-B27558. BRG1 is a homologue of the Drosophila
CC protein brahma, and has been shown to be bound to retinoblastoma tumour
CC suppressor protein RB. The BRG1 coding sequence and protein can be used
CC in the diagnosis and treatment of cancer (for example by gene therapy);
CC particularly prostate cancer, to identify drugs useful in the treatment
CC of cancer and in the production of animal models for cancer. Sequences
CC AAC58849-C58873 are all primers used in the isolation and sequencing of
CC the BRG1 gene and its variants.
XX
SQ Sequence 20 BP; 6 A; 5 C; 5 G; 4 T; 0 other;

Query Match      82.0%; Score 16.4; DB 21; Length 20;
Best Local Similarity 94.4%; Pred. No. 22;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ctgacatcagtagcatct 19
   ||| |||||
DB 20 CTGGCATCAGTAGCATCT 3

RESULT 3
AAC65564
ID AAC65564 standard; DNA; 15 BP.
XX
AC AAC65564;
XX
DT 12-FEB-2001 (first entry)
XX
DE Human focal adhesion kinase antisense sequence #30.
XX
KW Human; focal adhesion kinase; FAK; signal transduction; cancer;
KW embryonic development disorder; angiogenic disorder; wound healing;
KW antisense; phosphorothioate; ss.
XX
OS Homo sapiens.
XX
PI US6133031-A.
XX
PN 17-OCT-2000.
XX
PD 19-AUG-1999; 99US-0377310.
XX
PF 19-AUG-1999; 99US-0377310.
XX
PR (ISIS-) ISIS PHARM INC.
XX
PA Monia BP, Gaarde WA;
XX
PI WPI; 2001-006141/01.
XX
PN New antisense compounds for inhibiting focal adhesion kinase
PT expression, especially useful for inhibiting retinal
PT neovascularization, or for diagnosing and treating e.g. colon cancer -
XX
PS Example 2; Column 25; 30pp; English.
XX
CC The present invention describes a number of phosphorothioate antisense
CC sequences to the human focal adhesion kinase (FAK) protein. This protein
CC is involved in integrin-mediated signal transduction, and is implicated
CC in cancer, particularly colon, breast and oral tumours, embryonic
CC development disorders, angiogenic disorders and wound healing. The
CC antisense sequences, including the one shown here, can be used in the
CC treatment of all of these.
XX
SQ Sequence 15 BP; 5 A; 3 C; 3 G; 4 T; 0 other;

Query Match      75.0%; Score 15; DB 22; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 tgacatcagtagcat 17
   |||||
DB 1 tgacatcagtagcat 15

RESULT 4
AAF95492/c
ID AAF95492 standard; DNA; 21 BP.
XX
AC AAF95492;
XX
DT 06-JUN-2001 (first entry)
```


XX DE Human gene single nucleotide polymorphism #253.
 XX KW Human: variant thrombospondin 1; variant thrombospondin 4; SNP;
 KW polymorphism; vascular disease; coronary artery disease; forensics;
 KW myocardial infarction; atherosclerosis; stroke; venous thromboembolism;
 KW pulmonary embolism; paternity test; ds.
 XX OS Homo sapiens.
 XX FH Key Location/Qualifiers
 FT Variation replace(11,A)
 FT /*tag= a
 FT /standard_name= "single nucleotide polymorphism"
 XX PN WO200118250-A2.
 XX PD 15-MAR-2001.
 XX PF 07-SEP-2000; 2000WO-US24503.
 XX PR 10-SEP-1999; 99US-0153357.
 XX PR 26-JUL-2000; 2000US-0220947.
 XX PR 16-AUG-2000; 2000US-0225724.
 XX PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
 XX PA (MILL-) MILLENNIUM PHARM INC.
 XX PI Lander ES, Gargill M, Ireland JS, Bolk S, Daley GO, McCarthy JJ;
 XX DR WPI; 2001-226749/23.
 XX Nucleic acids comprising single nucleotide polymorphisms, useful in
 PT applications such as forensics, paternity testing, medicine, genetic
 PT analysis and phenotype correlations to diseases such as diabetes and
 PT atherosclerosis -
 XX Examples; Page 67; 242pp; English.
 XX The present invention provides a method of diagnosing a vascular disease
 CC in an individual, involving determining the sequence at various
 CC polymorphic sites within the human thrombospondin 1 and thrombospondin 4
 CC genes. The sequences at a number of polymorphic sites are also provided
 CC in the specification. In particular, the method can be used in the
 CC diagnosis of atherosclerosis, myocardial infarction, coronary heart
 CC disease, stroke, peripheral vascular diseases, venous thromboembolism
 CC and pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also
 CC useful in forensics, paternity testing, genetic analysis and phenotype
 CC correlations to diseases. The present sequence is an example of one of
 CC the human gene SNPs shown in the specification.
 XX Sequence 21 BP; 7 A; 4 C; 7 G; 3 T; 0 other;
 XX
 XX Query Match 71.0%; Score 14.2; DB 22; Length 21;
 XX Best Local Similarity 84.2%; Pred. No. 2.9e+02;
 XX Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 cctgacatcagtagcatct 19
 DB 19 CTTGCCATCAGTGGCATCT 1
 XX
 XX RESULT 5
 XX AAA51849/C
 XX ID AAA51849 standard; DNA; 39 BP.
 XX AC AAA51849;
 XX 09-JAN-2001 (first entry)
 XX Primer mcl-like-2f for human MC-R1 exon 2 amplification.
 XX

KW MC-R1; melanocortin 1 receptor; rhodopsin; G-protein coupled receptor;
 KW splice variant; MC-R1B; C-terminal extension; agonist; antagonist;
 KW modulator; PCR primer; ss.
 XX Homo sapiens.
 XX OS
 XX PN WO200039147-A1.
 XX PD 06-JUL-2000.
 XX PF 16-DEC-1999; 99WO-US29963.
 XX PR 23-DEC-1998; 98US-0113401.
 XX PA (MERI) MERCK & CO INC.
 XX PI Howard AD, MacNeil DJ, Van Der Ploeg LHT;
 XX DR WPI; 2000-452365/39.
 XX New nucleic acid encoding a human melanocortin 1 receptor protein
 PT (MC-R1B) for determining whether a substance is capable of binding to
 PT or activating human MC-R1B and identifying a substance that modulates
 PT MC-R1B receptor activity
 XX Example 1; Page 49; 101pp; English.
 XX The invention concerns novel splice variants of the melanocortin 1
 CC receptor (MC-R1) protein belonging to the rhodopsin sub-family of
 CC G-protein coupled receptors. The splice variants, referred to as MC-R1B
 CC proteins, contain an intracellular domain with an additional 65 amino
 CC acid residues in comparison to previously disclosed human MC-R1, referred
 CC to as MC-R1A. Additionally, residue 317 of the MC-R1B proteins is Cys,
 CC whereas the C-terminal amino acid residue 317 of known MC-R1A proteins is
 CC Trp. The novel sequences can be used to determine whether a substance
 CC modulates MC-R1B receptor activity and to identify potential agonists or
 CC antagonists of MC-R1B. Pharmaceutical compositions comprising
 CC modulators of MC-R1B are used to treat or diagnose disorders involving
 CC inappropriate melanocortin expression or activity.
 XX Sequence 39 BP; 5 A; 16 C; 9 G; 9 T; 0 other;
 XX
 XX Query Match 68.0%; Score 13.6; DB 21; Length 39;
 XX Best Local Similarity 80.0%; Pred. No. 6.4e+02;
 XX Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1 cctgacatcagtagcatctc 20
 DB 22 CCTGAGAGCAGGAGCATGTC 3
 XX
 XX RESULT 6
 XX AAA51848
 XX ID AAA51848 standard; DNA; 40 BP.
 XX AC AAA51848;
 XX 09-JAN-2001 (first entry)
 XX Primer mcl-like-1r for human MC-R1 exon 1 amplification.
 XX
 XX MC-R1; melanocortin 1 receptor; rhodopsin; G-protein coupled receptor;
 KW splice variant; MC-R1B; C-terminal extension; agonist; antagonist;
 KW modulator; PCR primer; ss.
 XX Homo sapiens.
 XX OS
 XX PN WO200039147-A1.
 XX PD 06-JUL-2000.
 XX PF 16-DEC-1999; 99WO-US29963.

XX PR 23-DEC-1998; 98US-0113401.
 XX PA (MERI) MERCK & CO INC.
 XX PI Howard AD, MacNeil DJ, Van Der Ploeg LHT;
 XX WPI; 2000-452365/39.
 XX
 XX New nucleic acid encoding a human melanocortin 1 receptor protein
 PT (MC-R1B) for determining whether a substance is capable of binding to
 PT or activating human MC-R1B and identifying a substance that modulates
 PT MC-R1B receptor activity
 XX
 XX Example 1; Page 49; 101pp; English.
 XX
 XX The invention concerns novel splice variants of the melanocortin 1
 CC receptor (MC-R1) protein belonging to the rhodopsin sub-family of
 CC G-protein coupled receptors. The splice variants, referred to as MC-R1B
 CC proteins, contain an intracellular domain with an additional 65 amino
 CC acid residues in comparison to previously disclosed human MC-R1, referred
 CC to as MC-R1A. Additionally, residue 317 of the MC-R1B proteins is Cys,
 CC whereas the C-terminal amino acid residue 317 of known MC-R1A proteins is
 CC Trp. The novel sequences can be used to determine whether a substance
 CC modulates MC-R1B receptor activity and to identify potential agonists or
 CC antagonists of MC-R1B. Pharmaceutical compositions comprising
 CC modulators of MC-R1B are used to treat or diagnose disorders involving
 CC inappropriate melanocortin expression or activity.
 XX
 XX Sequence 40 BP; 8 A; 12 C; 13 G; 7 T; 0 other;

Query Match 68.0%; Score 13.6; DB 21; Length 40;
 Best Local Similarity 80.0%; Pred. No. 6.4e+02;
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 cctgacatcagtagcatctc 20
 ||||| ||| ||||| ||
 Db 9 cctgagagcaggagcatgtc 28

RESULT 7
 AAQ23448/C
 ID AAQ23448 standard; DNA; 42 BP.
 AC AAQ23448;
 XX
 XX 17-AUG-1992 (first entry)
 DT
 XX Human heavy chain J region specific oligonucleotide.
 DE
 XX Placental; probe; heavy chain; ss.
 KW
 XX Synthetic.
 OS
 XX WO9203918-A.
 PN
 XX 19-MAR-1992.
 PD
 XX 28-AUG-1991; 91WO-US06185.
 PF
 XX 31-AUG-1990; 90US-0575962.
 PR
 XX 29-AUG-1990; 90US-0574748.
 PR
 XX (GENP-) GENPHARM INT INC.
 PA
 XX Lonberg N, Kay R;
 PI
 XX WPI; 1992-113962/14.
 DR
 XX Immunoglobulin trans:genes - for prodn. of heterologous
 PT non-rearranged and/or rearranged Ig chains
 PT
 XX

PS Example 14; Page 82; 172pp; English.

XX A human placental genomic DNA library cloned into the phage vector
 CC lambda EMBL3/SP6/T7 was screened with the human heavy chain J region
 CC specific oligonucleotide probe and the phage clone lambda 1.3 isolated.
 CC A 6 kb HindIII/KpnI fragment from this clone, contg. all six J segments
 CC as well as D segment BQ52 and the heavy chain J-mu intronic enhancer
 CC was isolated, and ultimately used to construct an Igm expressing
 CC mini-locus transgene.
 CC See also Q23419-50, Q22417-30.
 XX
 XX Sequence 42 BP; 5 A; 8 C; 15 G; 14 T; 0 other;

SQ

Query Match 68.0%; Score 13.6; DB 13; Length 42;
 Best Local Similarity 80.0%; Pred. No. 6.4e+02;
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 cctgacatcagtagcatctc 20
 || ||||| ||||| ||
 Db 35 CCAGACATCAAAAGCATCAC 16

RESULT 8
 AAQ44160/C
 ID AAQ44160 standard; DNA; 42 BP.
 XX
 XX AAQ44160;
 AC
 XX

DT 10-NOV-1993 (first entry)

XX Probe to isolate human immunoglobulin Joining segments.
 DE
 XX Immunoglobulin; Ig; heavy chain; minilocus; isotype switching;
 KW J region; ss.
 KW
 XX Synthetic.
 OS
 XX WO9312227-A.
 PN
 XX 24-JUN-1993.
 PD
 XX 17-DEC-1992; 92WO-US10983.
 PF
 XX 17-DEC-1991; 91US-0810279.
 PR
 XX 18-MAR-1992; 92US-0853408.
 PR
 XX 23-JUN-1992; 92US-0904068.
 PR
 XX (GENP-) GENPHARM INT INC.
 PA
 XX Kay RM, Lonberg N;
 PI
 XX WPI; 1993-214169/26.
 DR
 XX Transgenic non-human animals contg. immunoglobulin heavy chain
 PT trans gene - used to produce useful antibodies by isotype
 PT switching
 PT
 XX Example 4; Page 60; 196pp; English.

XX A 6.3kb BamHI/HindIII fragment that includes all J segments was
 CC isolated from human genomic DNA library using probe AAQ44160. An
 CC adjacent 10kb HindIII/BamHI fragment that contains enhancer, switch
 CC and constant region coding exons was similarly isolated using the
 CC probe AAQ44161 and an adjacent 3' 1.5kb BamHI fragment was isolated
 CC using pMUM insert as probe and cloned into pUC19. (pMUM is a 4kb
 CC EcoRI/HindIII fragment isolated from human genomic DNA library with
 CC oligonucleotide AAQ44162 mu membrane exon 1). All three fragments are
 CC used in the construction of plasmid pHIG1 which contains an 18kb
 CC insert encoding J and C-mu segments.
 XX
 XX Sequence 42 BP; 5 A; 8 C; 15 G; 14 T; 0 other;

SQ

```

Query Match      68.0%; Score 13.6; DB 14; Length 42;
Best Local Similarity 80.0%; Pred. No. 6.4e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 cctgacatcagtagcatctc 20
   || ||||| ||||| |
Db 35 CCAGACATCAAAAGCATCAC 16

RESULT 9
AAQ44180/c
ID AAQ44180 standard; DNA; 42 BP.
XX
AC AAQ44180;
XX
DT 10-NOV-1993 (first entry)
XX
DE Probe specific for human heavy chain J region.
XX
KW Immunoglobulin; IgM; heavy chain; minilocus transgene;
KW isotype switching; J-mu constant region; Joining region; ss.
XX
OS Synthetic.
XX
PN W09312227-A.
XX
PD 24-JUN-1993.
XX
PF 17-DEC-1992; 92WO-US10983.
XX
PR 17-DEC-1991; 91US-0810279.
PR 18-MAR-1992; 92US-0853408.
PR 23-JUN-1992; 92US-0904068.
XX
PA (GENP-) GENPHARM INT INC.
XX
PI Kay RM, Lonberg N;
XX
DR WPI; 1993-214169/26.
XX
PT Transgenic non-human animals contg. immunoglobulin heavy chain
PT trans gene - used to produce useful antibodies by isotype
PT switching
XX
PS Example 12; Page 91; 196pp; English.
XX
CC A human placental genomic DNA library cloned into the phage vector
CC lambda EMBL3/SP6/T7 was screened with the human heavy chain
CC J-region specific oligonucleotide Q44180. Phage clone lambda 1.3 was
CC isolated. A 6kb HindIII/KpnI fragment from this clone, containing
CC all 6 J segments as well as D segment DHQ52 and the heavy chain
CC J-mu intronic enhancer, was isolated. The same library was screened
CC with the human mu specific oligonucleotide Q44181 and phage clone
CC lambda 2.1 isolated. A 10.5kb HindIII/XhoI fragment, containing the
CC mu switch region and all of the mu constant region exons, was
CC isolated from this clone. The two fragments were ligated together
CC with KpnI/XhoI digested pNN03 to obtain plasmid pJMI which was used
CC in the construction of IgM expressing minilocus transgene pIGM1.
XX
SQ Sequence 42 BP; 5 A; 8 C; 15 G; 14 T; 0 other;

Query Match      68.0%; Score 13.6; DB 14; Length 42;
Best Local Similarity 80.0%; Pred. No. 6.4e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 cctgacatcagtagcatctc 20
   || ||||| ||||| |
Db 35 CCAGACATCAAAAGCATCAC 16

RESULT 10

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AAT37238/C
ID AAT37238 standard; DNA; 42 BP.
XX
AC AAT37238;
XX
DT 18-APR-1997 (first entry)
XX
DE Human antibody heavy chain J region specific probe.
XX
KW Heavy chain; J region; human; probe; minilocus; transgene;
KW transgenic; mouse; production; heterologous; antibody; IgM;
KW immunoglobulin; ss.
XX
OS Synthetic.
XX
PN US5545806-A.
XX
PD 13-AUG-1996.
XX
PF 29-AUG-1990; 90US-0574748.
XX
PR 16-DEC-1992; 92US-0990860.
PR 29-AUG-1990; 90US-0574748.
PR 31-AUG-1990; 90US-0575962.
PR 17-DEC-1991; 91US-0810279.
PR 18-MAR-1992; 92US-0853408.
PR 23-JUN-1992; 92US-0904068.
XX
PA (GENP-) GENPHARM INT INC.
XX
PI Kay RM, Lonberg N;
XX
DR WPI; 1996-383736/38.
XX
PT Prodn. of heterologous human immunoglobulin(s) - by immunising
PT transgenic mice
XX
PS Example 12; Columns 57-58; 94pp; English.
XX
CC The present sequence is a probe specific for a human antibody heavy
CC chain J region, which was used in the construction of a IgM heavy
CC chain minilocus transgene. The transgene was injected into mouse
CC embryo pronuclei to generate transgenic mice, which can be used for
CC the production of heterologous (i.e. human) antibodies against
CC specific antigens, this comprises immunising a mouse with a
CC preselected antigen and collecting antigen binding heterologous
CC human IgM immunoglobulins.
XX
SQ Sequence 42 BP; 5 A; 8 C; 15 G; 14 T; 0 other;

Query Match      68.0%; Score 13.6; DB 17; Length 42;
Best Local Similarity 80.0%; Pred. No. 6.4e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 cctgacatcagtagcatctc 20
   || ||||| ||||| |
Db 35 CCAGACATCAAAAGCATCAC 16

RESULT 11
AAT37216/C
ID AAT37216 standard; DNA; 42 BP.
XX
AC AAT37216;
XX
DT 18-APR-1997 (first entry)
XX
DE Human antibody J segment oligonucleotide probe.
XX
KW Heavy chain; gene segment; human; DNA fragment; probe;
KW minilocus; transgenic; mouse; J segment;
KW production; heterologous; antibody; gamma; immunoglobulin; ss.

```



```

XX Synthetic.
OS Homo sapiens.
XX
XX US5633425-A.
XX
XX 27-MAY-1997.
XX
XX 05-FEB-1992; 92US-0834539.
XX
XX 29-AUG-1990; 90US-0574448.
XX
XX 31-AUG-1990; 90US-0575962.
XX
XX (GENP-) GENPHARM INT INC.
XX
XX Kay RM, Lonberg N;
XX
XX WPI; 1997-297410/27.
XX
XX Transgenic mouse for heterologous antibody production - containing
XX DNA encoding human immunoglobulin components
XX
XX Example 5; Column 33; 90pp; English.
XX
XX This oligonucleotide was used as a probe to facilitate in the
XX cloning of a J-mu region from a human immunoglobulin. The probe
XX isolated a 6.3 kb BamHI/HindIII fragment from a human genomic library
XX which included all joining (J) segments. This region is used in a novel
XX method of developing transgenic non-human animals capable of producing
XX heterologous antibodies encoded by human immunoglobulin genes. Such
XX transgenically produced monoclonal antibodies should alleviate the
XX intrinsic immunogenicity of non-human immunoglobulins allowing the
XX development of new in vivo applications.
XX
XX Sequence 42 BP; 5 A; 8 C; 15 G; 14 T; 0 other;

Query Match 68.0%; Score 13.6; DB 18; Length 42;
Best Local Similarity 80.0%; Pred. No. 6.4e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 cctgacatcagtagcatctc 20
   || ||||| ||||| |
DB 35 CCAGACATCAAAAGCATCAC 16

RESULT 14
AAT73468/C
ID AAT73468 standard; DNA; 42 BP.
XX
XX AAT73468;
XX
XX 23-JAN-1998 (first entry)
XX
XX Human heavy chain J region specific probe.
XX
XX Ig; affinity constant; human; antigen; hybridoma; B cell; transgene;
XX transgenic; mouse; CD4; antibody; autoimmune; inflammatory;
XX transplant rejection; immunoglobulin; ss.
XX
XX Synthetic.
XX OS Homo sapiens.
XX
XX WO9713852-A1.
XX
XX 17-APR-1997.
XX
XX 10-OCT-1996; 96WO-US16433.
XX
XX 10-OCT-1995; 95US-0544404.
XX
XX (GENP-) GENPHARM INT INC.
XX
XX Kay RM, Lonberg N;
XX
XX WPI; 1997-297410/27.
XX
XX Novel anti-CD4 antibody produced by transgenic mice - used in the
XX treatment of auto-immune disease etc.
XX
XX Example 4; Page 103; 396pp; English.
XX
XX A novel composition has been developed which comprises an immunoglobulin
XX (Ig) having an affinity constant (Ka) of at least 2 multiply
XX present sequence represents a probe used to screen a human placental
XX genomic DNA library cloned into the phage vector lambdaEMBL3/SP6/T7,
XX for the human heavy chain J region. Anti-CD4 antibodies may be used in
XX therapeutic and diagnostic applications, especially for the treatment
XX of human diseases. These antibodies reduce activity of CD4 cells and
XX reduce undesirable autoimmune reactions, inflammatory response and
XX transplant rejection. Transgenic animals are capable of producing
XX heterologous antibodies of multiple isotypes by undergoing isotype
XX switching. These animals produce a first Ig type that is necessary for
XX antigen-stimulated B-cell maturation and can switch to encode and
XX produce one or more subsequent heterologous isotypes.
XX
XX Sequence 42 BP; 5 A; 8 C; 15 G; 14 T; 0 other;

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```

PI Kay RM, Lonberg N;
XX
XX WPI; 1997-235888/21.
XX
XX Novel anti-CD4 antibody produced by transgenic mice - used in the
XX treatment of auto-immune disease etc.
XX
XX Example 12; Page 133; 396pp; English.
XX
XX A novel composition has been developed which comprises an immunoglobulin
XX (Ig) having an affinity constant (Ka) of at least 2 multiply
XX 100000000 M-1 for binding to a predetermined human antigen. The
XX present sequence represents a probe used to screen a human placental
XX genomic DNA library cloned into the phage vector lambdaEMBL3/SP6/T7,
XX for the human heavy chain J region. Anti-CD4 antibodies may be used in
XX therapeutic and diagnostic applications, especially for the treatment
XX of human diseases. These antibodies reduce activity of CD4 cells and
XX reduce undesirable autoimmune reactions, inflammatory response and
XX transplant rejection. Transgenic animals are capable of producing
XX heterologous antibodies of multiple isotypes by undergoing isotype
XX switching. These animals produce a first Ig type that is necessary for
XX antigen-stimulated B-cell maturation and can switch to encode and
XX produce one or more subsequent heterologous isotypes.
XX
XX Sequence 42 BP; 5 A; 8 C; 15 G; 14 T; 0 other;

Query Match 68.0%; Score 13.6; DB 18; Length 42;
Best Local Similarity 80.0%; Pred. No. 6.4e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 cctgacatcagtagcatctc 20
   || ||||| ||||| |
DB 35 CCAGACATCAAAAGCATCAC 16

RESULT 15
AAT73448/C
ID AAT73448 standard; DNA; 42 BP.
XX
XX AAT73448;
XX
XX 03-DEC-1997 (first entry)
XX
XX Human J-mu region genomic DNA library probe.
XX
XX Ig; affinity constant; human; antigen; hybridoma; B cell; transgene;
XX transgenic; mouse; CD4; antibody; autoimmune; inflammatory;
XX transplant rejection; ss.
XX
XX Synthetic.
XX OS Homo sapiens.
XX
XX WO9713852-A1.
XX
XX 17-APR-1997.
XX
XX 10-OCT-1996; 96WO-US16433.
XX
XX 10-OCT-1995; 95US-0544404.
XX
XX (GENP-) GENPHARM INT INC.
XX
XX Kay RM, Lonberg N;
XX
XX WPI; 1997-235888/21.
XX
XX Novel anti-CD4 antibody produced by transgenic mice - used in the
XX treatment of auto-immune disease etc.
XX
XX Example 4; Page 103; 396pp; English.
XX
XX A novel composition has been developed which comprises an immunoglobulin
XX (Ig) having an affinity constant (Ka) of at least 2 multiply

```

CC 1000000000 M-1 for binding to a predetermined human antigen. The
 CC present sequence represents a probe used for the isolation of human
 CC J segments from a human genomic DNA library. The anti-CD4 antibodies
 CC may be used in therapeutic and diagnostic applications, especially for
 CC the treatment of human diseases. These antibodies reduce activity of
 CC CD4 cells and reduce undesirable autoimmune reactions, inflammatory
 CC response and transplant rejection. Transgenic animals are capable of
 CC producing heterologous antibodies of multiple isotypes by undergoing
 CC isotype switching. These animals produce a first Ig type that is
 CC necessary for antigen-stimulated B-cell maturation and can switch to
 CC encode and produce one or more subsequent heterologous isotypes.

XX Sequence 42 BP; 5 A; 8 C; 15 G; 14 T; 0 other;

Query Match 68.0%; Score 13.6; DB 18; Length 42;
 Best Local Similarity 80.0%; Pred. No. 6.4e+02;
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 cctgacatcagtagcatctc 20
 |||||||
 Db 35 CCAGACATCAAAAGCATCAC 16

Search completed: October 2, 2001, 16:18:41
 Job time: 15485 sec

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OM nucleic - nucleic search, using sw model

Run on: October 2, 2001, 16:03:49 ; Search time 417.38 Seconds
(without alignments)
9.071 Million cell updates/sec

Title: US-09-757-100B-11

Perfect score: 20

Sequence: 1 agtaccaggtagctcttag 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 324599 seqs, 9465562 residues

Total number of hits satisfying chosen parameters: 460742

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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5: /cgn2_6/ptodata/1/ina/PCRUS.COMB.seq.*

6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	3	US-09-377-310-11
2	15	75.0	15	3	US-09-377-310-31
c 3	13.4	67.0	21	1	US-08-136-118-7
c 4	12.8	64.0	27	4	US-09-246-277A-8
c 5	12.8	64.0	29	1	US-08-530-492-69
c 6	12.8	64.0	29	4	US-08-906-517-69
7	12.8	64.0	34	2	US-08-988-128-15
c 8	12.8	64.0	48	2	US-08-865-675-6
c 9	12.8	64.0	48	2	US-09-237-510-6
c 10	12.4	62.0	20	4	US-09-488-671-119
c 11	12.4	62.0	22	2	US-08-117-952-668
c 12	12.4	62.0	46	4	US-09-060-410-12
c 13	12.2	61.0	20	4	US-09-101-886B-71
14	12.2	61.0	32	3	US-08-685-871-14
15	12.2	61.0	32	3	US-08-685-871-27
16	12.2	61.0	32	3	US-08-685-871-31
17	12.2	61.0	32	3	US-08-685-871-33
18	12.2	61.0	32	3	US-08-685-871-41
19	12.2	61.0	32	3	US-08-685-871-43
c 20	12.2	61.0	44	2	US-07-916-098A-36
21	12.2	61.0	44	2	US-07-916-098A-59
22	12	60.0	20	2	US-08-609-443B-53
c 23	12	60.0	30	3	US-09-339-993-4
24	11.8	59.0	20	3	US-09-257-799-49
25	11.8	59.0	20	3	US-08-920-919A-49
26	11.8	59.0	41	2	US-08-818-604-8
c 27	11.6	58.0	26	1	US-08-482-882-87

c 28	11.6	58.0	26	1	US-08-483-389-87	Sequence 87, Appl
c 29	11.6	58.0	26	2	US-08-487-113D-87	Sequence 87, Appl
c 30	11.6	58.0	26	2	US-08-473-503-87	Sequence 87, Appl
c 31	11.6	58.0	26	2	US-08-483-932-87	Sequence 87, Appl
c 32	11.6	58.0	26	2	US-08-720-420A-87	Sequence 87, Appl
c 33	11.6	58.0	26	2	US-08-859-998-95	Sequence 95, Appl
c 34	11.6	58.0	26	3	US-08-714-017-87	Sequence 87, Appl
c 35	11.6	58.0	26	3	US-08-475-680-87	Sequence 87, Appl
c 36	11.6	58.0	40	1	US-08-482-882-100	Sequence 100, App
c 37	11.6	58.0	40	1	US-08-483-389-100	Sequence 100, App
c 38	11.6	58.0	40	2	US-08-487-113D-100	Sequence 100, App
c 39	11.6	58.0	40	2	US-08-473-503-100	Sequence 100, App
c 40	11.6	58.0	40	2	US-08-483-932-100	Sequence 100, App
c 41	11.6	58.0	40	2	US-08-720-420A-100	Sequence 100, App
c 42	11.6	58.0	40	3	US-08-714-017-100	Sequence 100, App
c 43	11.6	58.0	40	3	US-08-475-680-100	Sequence 100, App
c 44	11.6	58.0	42	1	US-07-834-539A-58	Sequence 58, Appl
c 45	11.6	58.0	42	5	PCT-US92-10983-106	Sequence 106, App

ALIGNMENTS

RESULT 1
US-09-377-310-11
; Sequence 11, Application US/09377310B
; Patent No. 6133031
; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P.
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
; TITLE OF INVENTION: Expression
; FILE REFERENCE: ISPH-0389
; CURRENT APPLICATION NUMBER: US/09/377,310B
; CURRENT FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
US-09-377-310-11

Query Match 100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.034;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 agtaccaggtagctcttag 20
|||||
Db 1 agtaccaggtagctcttag 20

RESULT 2
US-09-377-310-31
; Sequence 31, Application US/09377310B
; Patent No. 6133031
; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P.
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
; TITLE OF INVENTION: Expression
; FILE REFERENCE: ISPH-0389
; CURRENT APPLICATION NUMBER: US/09/377,310B
; CURRENT FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 31
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence

```

; FEATURE:
; OTHER INFORMATION: antisense sequence
US-09-377-310-31

Query Match 75.0%; Score 15; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 taccagggtgagct 17
Db 1 taccagggtgagct 15

RESULT 3
US-08-136-118-7/c
; Sequence 7, Application US/08136118
; Patent No. 5580969
; GENERAL INFORMATION:
; APPLICANT: HOKE, Glenn D
; APPLICANT: BRADLEY, Matthews O
; APPLICANT: WILLIAMS, Taffy J
; APPLICANT: LEE, Che-Hung
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES DIRECTED
; AGAINST HUMAN ICAM-1
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; STREET: 8901 Wisconsin Ave.
; CITY: Bethesda
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20889-5606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/136,118
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/918,259
; FILING DATE: 24-JUL-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Spevack, A. David
; REGISTRATION NUMBER: 24,743
; REFERENCE/DOCKET NUMBER: N.C. 75,776
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 295-6759
; TELEFAX: (202) 295-1022
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; HYPOTHETICAL: NO
; ANTI-SENSE: YES
US-08-136-118-7

Query Match 67.0%; Score 13.4; DB 1; Length 21;
Best Local Similarity 93.3%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 gtaccagggtgagtc 16
Db 19 GTTCCCGAGGTGAGTC 5

RESULT 4
US-09-246-277A-8/c
; Sequence 8, Application US/09246277A
; Patent No. 6238866
; GENERAL INFORMATION:
; APPLICANT: Veb, Homer R., Wick, Charles H.
; TITLE OF INVENTION: NOVEL DETECTOR FOR NUCLEIC ACID
; TYPING AND METHODS OF USING THE SAME
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Office of the Chief Counsel
; STREET: U.S. Army SBCCOM
; CITY: APG(EA)
; STATE: Maryland
; COUNTRY: United States of America
; ZIP: 21010-5423
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/246,277A
; FILING DATE: 08-Feb-1999
; CLASSIFICATION: <unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Biffoni, U. John
; REGISTRATION NUMBER: 39908
; REFERENCE/DOCKET NUMBER: 436-96
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (410) 436-1158
; TELEFAX: (410) 436-2534
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: EFD52 Minisatellite
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Query Match 64.0%; Score 12.8; DB 4; Length 27;
Best Local Similarity 70.0%; Pred. No. 2.5e+02;
Matches 14; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 agtaccagggtgagcttag 20
Db 22 AGTARCCAGGRSMGTGCTAG 3

RESULT 5
US-08-530-492-69/c
; Sequence 69, Application US/08530492
; Patent No. 5689052
; GENERAL INFORMATION:
; APPLICANT: Brown, Sherri M.
; APPLICANT: Dean, Duff A.
; APPLICANT: Fromm, Michael E.
; APPLICANT: Sanders, Patricia R.
; TITLE OF INVENTION: Synthetic DNA Sequences Having Enhanced
; Expression in Monocotyledonous Plants and Method For
; Preparation Thereof
; NUMBER OF SEQUENCES: 164
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. BB4F
; STREET: 700 Chesterfield Parkway No. 5689052th
```


CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63198
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/530,492
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/172,333
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Hoerner Jr., Dennis R.
REGISTRATION NUMBER: 30,914
REFERENCE/DOCKET NUMBER: 38-21(10605)A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)537-6099
TELEFAX: (314)537-6047
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (synthetic)
US-08-530-492-69

Query Match 64.0%; Score 12.8; DB 1; Length 29;
Best Local Similarity 87.5%; Pred. No. 2.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 agtaccagggtgagtc 16
||| ||||| |||||
Db 24 AGTCCCCAGGAGAGTC 9

RESULT 6
US-08-906-517-69/c
Sequence 69, Application US/08906517
Patent No. 6180774
GENERAL INFORMATION:
APPLICANT: Brown, Sherri M.
APPLICANT: Dean, Duff A.
APPLICANT: Fromm, Michael E.
APPLICANT: Sanders, Patricia R.
TITLE OF INVENTION: Synthetic DNA Sequences Having Enhanced
TITLE OF INVENTION: Expression in Monocotyledonous Plants and Method For
TITLE OF INVENTION: Preparation Thereof
NUMBER OF SEQUENCE ADDRESSES: 164
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Arnold, White & Durkee
STREET: P. O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/906,517
FILING DATE: Concurrently Herewith
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.

REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: MOBT:170
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577 69:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-906-517-69

Query Match 64.0%; Score 12.8; DB 4; Length 29;
Best Local Similarity 87.5%; Pred. No. 2.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 agtaccagggtgagtc 16
||| ||||| |||||
Db 24 AGTCCCCAGGAGAGTC 9

RESULT 7
US-08-988-128-15
Sequence 15, Application US/08988128
Patent No. 5994505
GENERAL INFORMATION:
APPLICANT: Ting, Jenny Pan-Yung
APPLICANT: Chin, Keh-Chin
TITLE OF INVENTION: No. 5994505el Forms of Class II MHC
TITLE OF INVENTION: Transactivator (CIITA)
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Myers Bigel Sibley & Sajovec, P.A.
STREET: P.O. Box 37428
CITY: Raleigh
STATE: No. 5994505th Carolina
COUNTRY: USA
ZIP: 27627
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/988,128
FILING DATE: 10-DEC-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Biswas, Sorojini J.
REGISTRATION NUMBER: 39,111
REFERENCE/DOCKET NUMBER: 5470-136
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 854-1400
TELEFAX: (919) 854-1401
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-988-128-15

Query Match 64.0%; Score 12.8; DB 2; Length 34;
Best Local Similarity 87.5%; Pred. No. 2.6e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 taccagggtgagtcctt 18
||| ||||| || |||||
Db 16 TACCAGCTGTGTCTT 31

STREET: 444 South Flower Street, Suite 2000
CITY: Los Angeles
STATE: CA
COUNTRY: USA
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/117,952
FILING DATE: 07-SEP-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/078,471
FILING DATE: 15-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Reiter, Stephen E.
REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P41 9423
TELEPHONE: 619-546-4737
TELEFAX: 619-546-9392
INFORMATION FOR SEQ ID NO: 668:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Oligonucleotide
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-117-952-668

Query Match 62.0%; Score 12.4; DB 2; Length 22;
Best Local Similarity 92.9%; Pred. No. 4e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 acccaggtgagctt 17
| | | | | | | | | |
DB 14 ATCCAGGTGAGTCT 1

RESULT 12
US-09-060-410-12/c
Sequence 12, Application US/09060410
Patent No. 6165461
GENERAL INFORMATION:
APPLICANT: Cobb, Melanie
APPLICANT: Hutchinson, Michele
APPLICANT: Chen, Zhu
APPLICANT: Berman, Kevin
TITLE OF INVENTION: TAO PROTEIN KINASES AND METHODS OF USE
TITLE OF INVENTION: THEREFOR
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/060,410
FILING DATE: 14-APR-1998
CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 860098.421
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 46 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-060-410-12

Query Match 62.0%; Score 12.4; DB 4; Length 46;
Best Local Similarity 92.9%; Pred. No. 4.4e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 agtaccaggtgag 14
| | | | | | | | | |
DB 14 AGTACCCAGGTGAG 1

RESULT 13
US-09-101-886B-71
Sequence 71, Application US/09101886B
Patent No. 6197507
GENERAL INFORMATION:
APPLICANT: BERG, THOMAS
APPLICANT: TOLLERSRUD, OLE K
APPLICANT: NILSEN, OIVIND
TITLE OF INVENTION: GENETIC TEST FOR ALPHA-MANNOSIDOSIS
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: BARBARA G. ERNST
STREET: 555 13TH STREET, NW SUITE 701E
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/101,886B
FILING DATE: 29-JANUARY-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB97/00109
FILING DATE: 12-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: ERNST, BARBARA G
REGISTRATION NUMBER: 30,377
REFERENCE/DOCKET NUMBER: 1181-240
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-783-6040
TELEFAX: 202-783-6031
INFORMATION FOR SEQ ID NO: 71:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-09-101-886B-71

Query Match 61.0%; Score 12.2; DB 4; Length 20;
Best Local Similarity 82.4%; Pred. No. 5.1e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 agtaccaggtagctt 17
| | ||||| | | | | |
Db 2 AATGCCAGGTGAGTGT 18

RESULT 14
US-08-685-871-14
; Sequence 14, Application US/08685871
; Patent No. 6013499
; GENERAL INFORMATION:
; APPLICANT: NARUMIYA, Shuh
; APPLICANT: IWAMATSU, Akihiro
; TITLE OF INVENTION: RHO TARGET PROTEIN KINASE P160
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/685.871
; FILING DATE: 24-JUL-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 8-184102
; FILING DATE: 25-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-262553
; FILING DATE: 14-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 16887/845
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-685-871-14

Query Match 61.0%; Score 12.2; DB 3; Length 32;
Best Local Similarity 82.4%; Pred. No. 5.4e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 acccaggtagctttag 20
| | | | | | | | | | | | | | | |
Db 3 ACCCGGTGTGTATTAG 19

RESULT 15
US-08-685-871-27
; Sequence 27, Application US/08685871
; Patent No. 6013499
; GENERAL INFORMATION:
; APPLICANT: NARUMIYA, Shuh
; APPLICANT: IWAMATSU, Akihiro

; TITLE OF INVENTION: RHO TARGET PROTEIN KINASE P160
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/685.871
; FILING DATE: 24-JUL-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 8-184102
; FILING DATE: 25-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-262553
; FILING DATE: 14-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 16887/845
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-685-871-27

Query Match 61.0%; Score 12.2; DB 3; Length 32;
Best Local Similarity 82.4%; Pred. No. 5.4e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 acccaggtagctttag 20
| | | | | | | | | | | | | | | |
Db 3 ACCCGGTGTGTATTAG 19

Search completed: October 2, 2001, 16:03:49
Job time: 14593 sec

XXI

PS Claim 15; Column 23; 30pp; English.

XX The present invention describes a number of phosphorothioate antisense
CC sequences to the human focal adhesion kinase (FAK) protein. This protein
CC is involved in integrin-mediated signal transduction, and is implicated
CC in cancer, particularly colon, breast and oral tumours, embryonic
CC development disorders, angiogenic disorders and wound healing. The
CC antisense sequences, including the one shown here, can be used in the
CC treatment of all of these.

XX Sequence 20 BP; 5 A; 4 C; 6 G; 5 T; 0 other;

Query Match 100.0%; Score 20; DB 22; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 agtaccagggtgagctcttag 20
|||||

Db 1 agtaccagggtgagctcttag 20
|||||

RESULT 2

AAC65563
ID AAC65563 standard; DNA; 15 BP.

XX AAC65563;

DT 12-FEB-2001 (first entry)

DE Human focal adhesion kinase antisense sequence #29.

XX Human; focal adhesion kinase; FAK; signal transduction; cancer;
KW embryonic development disorder; angiogenic disorder; wound healing;
KW antisense; phosphorothioate; ss.

XX Homo sapiens.

XX US6133031-A.

PD 17-OCT-2000.

XX 19-AUG-1999; 99US-0377310.

XX 19-AUG-1999; 99US-0377310.

XX (ISIS-) ISIS PHARM INC.

XX Monia BP, Gaarde WA;

XX WPI; 2001-006141/01.

XX New antisense compounds for inhibiting focal adhesion kinase
PT expression, especially useful for inhibiting retinal
PT neovascularization, or for diagnosing and treating e.g. colon cancer -

XX Claim 15; Column 25; 30pp; English.

XX The present invention describes a number of phosphorothioate antisense
CC sequences to the human focal adhesion kinase (FAK) protein. This protein
CC is involved in integrin-mediated signal transduction, and is implicated
CC in cancer, particularly colon, breast and oral tumours, embryonic
CC development disorders, angiogenic disorders and wound healing. The
CC antisense sequences, including the one shown here, can be used in the
CC treatment of all of these.

XX Sequence 15 BP; 3 A; 4 C; 4 G; 4 T; 0 other;

Query Match 75.0%; Score 15; DB 22; Length 15;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 taccagggtgagctct 17
|||||

Db 1 taccagggtgagctct 15
|||||

RESULT 3

AAT58077/C
ID AAT58077 standard; DNA; 21 BP.

XX AAT58077;

XX 18-MAR-1997 (first entry)

DE ICAM-1 antisense oligonucleotide #7.

XX Antisense; pre-mRNA; mature mRNA; vascular defect; tissue defect;
KW human intercellular adhesion molecule-1; ICAM-1; inflammation;
KW adult respiratory distress syndrome; multiple organ failure; GM1594;
KW septic shock; ss.

XX Synthetic.

XX US5580969-A.

XX 03-DEC-1996.

XX 24-JUL-1992; 92US-0918259.

XX 12-OCT-1993; 93US-0136118.

XX 24-JUL-1992; 92US-0918259.

XX (USNA) US SEC OF NAVY.

XX Bradley MO, Hoke GD, Lee C, Williams TJ;

XX WPI; 1997-033603/03.

XX Anti-sense oligo:nucleotide(s) for blocking ICAM-1 mRNA translation
PT - for treating septic shock, adult respiratory distress syndrome
PT etc.

XX Claim 1; Column 21; 16pp; English.

XX The sequences given in AAT58071-85 represent oligonucleotides which are
CC antisense to sequences contained in the pre-mRNA or mature mRNA
CC transcript of human intercellular adhesion molecule-1 (ICAM-1).
CC These oligonucleotides may be used for treating septic shock and the
CC manifestations of septic shock, e.g. inflammation, and vascular and
CC tissue defects. They are also useful in the treatment of septic
CC shock associated diseases, e.g. adult respiratory distress syndrome,
CC multiple organ failure etc.

XX Sequence 21 BP; 5 A; 9 C; 5 G; 2 T; 0 other;

Query Match 67.0%; Score 13.4; DB 18; Length 21;
Best Local Similarity 93.3%; Pred. No. 5.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 gtaccagggtgagtc 16
|||||

Db 19 GTTCCCGAGGTGAGTC 5
|||||

RESULT 4

AAV38613/C
ID AAV38613 standard; DNA; 21 BP.

XX AAV38613;

XX 13-OCT-1998 (first entry)

DE Human ICAM-1, E-selectin, VCAM-1 antisense oligonucleotide.


```

XX ICAM-1; intracellular adhesion molecule-; E-selectin; VCAM-1;
KW vascular cell adhesion molecule-1; antisense; inflammatory;
KW disease; treatment; septic shock; psoriasis; wounds; burns; acne;
KW arthritis; organ rejection; inhibition; expression; ss.
XX
OS Synthetic.
OS Homo sapiens.
PN WO9824797-A1.
XX
XX 11-JUN-1998.
PD
XX
XX 02-DEC-1996; 96WO-US19194.
XX
XX 02-DEC-1996; 96WO-US19194.
PR
XX
XX (DYAD-) DYAD PHARM CORP.
PA
XX
XX Bradley MO, Hoke GD, Lee C, Williams TJ;
PI
XX
XX WPI; 1998-333253/29.
DR
XX
XX Antisense oligonucleotides to ICAM-1, E-selectin or VCAM-1 - useful
PT for treating diseases having an inflammatory component, e.g.
PT psoriasis, wounds and septic shock
PT
XX
XX Claim 8; Page 40; 48pp; English.
PS
XX
XX The sequence is that of an antisense oligonucleotide which is
CC substantially complementary to at least a portion of the pre-
CC or mature RNA transcript of human intracellular adhesion molecule
CC (ICAM), E-selectin or vascular cell adhesion molecule (VCAM).
CC It can be used to inhibit expression of these proteins. Inhibition
CC of these proteins forms the basis for treatment of conditions and
CC diseases that have an inflammatory component, e.g. acne, psoriasis,
CC arthritis, organ rejection, wounds, burns, septic shock or
CC inflammatory complications of septic shock.
XX
XX Sequence 21 BP; 5 A; 9 C; 5 G; 2 T; 0 other;
SQ

```

```

XX (KIRI ) KIRIN BEER KK.
PA
XX
XX Ishida I, Tomizuka K, Kuroiwa Y, Ohshima T, Suzuki M, Itoh K;
PI
XX
XX WPI; 2001-202806/20.
DR
XX
XX Mouse having completely humanized human cytochrome P450 gene for use in
PT studying drug efficacy, metabolism and toxicity with ease -
PT
XX
XX Example 16; Page 67; 137pp; Japanese.
PS
XX
XX This invention relates to a mouse containing the human cytochrome P450
CC gene (from the CYP3A family). PCR primers AAF92356 - AAF92441 are used
CC in examples illustrating the construction of vectors used in the
CC production of the transgenic mouse of the invention. The mouse can be
CC used for studying human drug efficacy, metabolism and toxicity, including
CC the application of immortalised cell and tissue cultures.
XX
XX Sequence 36 BP; 8 A; 7 C; 8 G; 13 T; 0 other;
SQ

```

```

Query Match 66.0%; Score 13.2; DB 22; Length 36;
Best Local Similarity 83.3%; Pred. No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 gtaccacagtgagtcctta 19
Db 6 gtaccacagtcaggctta 23

RESULT 6
AAAF92420
ID AAA10299 standard; DNA; 23 BP.
XX
AC AAA10299;
XX
XX 03-JUL-2000 (first entry)
XX
XX HIV-1 LTR (long terminal repeat) PCR primer, SEQ ID NO:4.
XX
XX Long terminal repeat; LTR; HIV-1; APJ receptor; coreceptor;
KW cellular infection; envelope protein; env; CD4 coexpression;
KW drug development; PCR primer; ss.
XX
XX Human immunodeficiency virus type 1.
OS
XX
XX WO200014220-A1.
PN
XX
XX 16-MAR-2000.
PD
XX
XX 07-SEP-1999; 99WO-EP06553.
PF
XX
XX 08-SEP-1998; 98US-0149045.
PR
XX
XX (SCHD ) SCHERING AG.
PA
XX
XX Doms R, Faulds D, Hesselgesser JE, Horuk R, Mitrovic B, Zhou Y;
PI
XX
XX WPI; 2000-256972/22.
DR
XX
XX New recombinant eukaryotic cells coexpressing APJ and CD4 polypeptides,
PT useful for identifying compounds that modulate interaction between an
PT HIV virus and an APJ receptor e.g. to develop anti-HIV drugs -
PT
XX
XX Example 2; Page 36; 67pp; English.
PS
XX
XX The invention relates to recombinant eukaryotic cells transformed with a
CC nucleotide encoding an APJ protein and/or a nucleotide encoding the CD4
CC protein, such that the cells coexpress APJ and CD4. The APJ receptor
CC (AAF97466) is an orphan seven transmembrane domain receptor that has
CC been found to function as an efficient coreceptor for cellular infection
CC by a number of HIV-1 and SIV strains. The entry of HIV into cells
CC

```

```

Query Match 67.0%; Score 13.4; DB 19; Length 21;
Best Local Similarity 93.3%; Pred. No. 5.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 gtaccacagtgagtc 16
Db 19 GTTCCAGGTGAGTC 5

RESULT 5
AAAF92420
ID AAF92420 standard; DNA; 36 BP.
XX
AC AAF92420;
XX
XX 16-MAY-2001 (first entry)
DT
XX
XX Pro alpha 2 (I) collagen (COL1A2) specific PCR primer SEQ ID 65.
DE
XX
XX Human; cytochrome P450; Cyp3A; PCR primer; transgenic mouse;
KW immortalised cell; ss.
KW
XX
XX Homo sapiens.
OS
XX
XX WO200111951-A1.
PN
XX
XX 22-FEB-2001.
PD
XX
XX 11-AUG-2000; 2000WO-JP05424.
PF
XX
XX 13-AUG-1999; 99JP-0229094.
PR

```

CC involves binding of the viral envelope protein (env) to CD4, followed by
 CC interaction with a coreceptor. Binding to the coreceptor triggers a
 CC conformational change in env that mediates fusion between the viral
 CC membrane and the host cell membrane. The invention also encompasses
 CC peptides and antibodies which specifically bind to an extracellular
 CC domain of APJ. These inhibit membrane fusion between a cell coexpressing
 CC the APJ and CD4 proteins and a cell expressing an HIV env protein and
 CC thereby inhibits HIV infection of the APJ/CD4-expressing cell. The new
 CC recombinant cells provide an important tool for investigating and
 CC controlling HIV infection. The cells can be used to identify compounds
 CC that modulate interaction between HIV and an APJ receptor, which may be
 CC useful in the development of anti-HIV drugs. Contacting cells expressing
 CC APJ and CD4 with an APJ binding/blocking agent (e.g., the antibodies or
 CC peptides) may be useful to inhibit HIV infection of such cells, e.g., to
 CC treat subjects having an HIV-related disorder associated with APJ
 CC expression. Antibodies and peptide fragments can be included in
 CC medicines and administered to treat patients (especially foetuses)
 CC having, or at risk of developing, an HIV infection or related disorder.
 CC The antibodies can also be used to detect cells expressing the APJ receptor,
 CC and are useful to diagnose susceptibility to HIV infection. For example,
 CC higher APJ levels in central nervous system tissues may indicate an
 CC increased risk of neuropathogenesis associated with HIV infection.
 CC Transgenic animals which express human CD4 and APJ proteins may provide
 CC model systems for the study of HIV infection and for anti-HIV drug
 CC development. Sequences AAA10299-A10300 represent PCR primers used in an
 CC exemplification of the present invention to amplify HIV-1 ITR (long
 CC terminal repeat) DNA sequences from CD4/APJ-expressing cells which had
 CC been previously exposed to HIV-1. The amplified ITR DNA was detected via
 CC hybridisation with a labelled probe (AAA10301).
 XX
 SQ Sequence 23 BP; 7 A; 7 C; 5 G; 4 T; 0 other;

Query Match 64.0%; Score 12.8; DB 21; Length 23;
 Best Local Similarity 87.5%; Pred. No. 1.1e+03;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 agtaccagggtgagtc 16
 ||||| |||||
 Db 8 agtaccagggtgagtc 23

RESULT 7
 AAA72481/c
 ID AAA72481 standard; DNA; 25 BP.
 XX
 AC AAA72481;
 XX
 DT 19-DEC-2000 (first entry)
 XX
 DE Soybean chalcone reductase PCR primer, SEQ ID NO:65.
 XX
 KW Soybean: chalcone reductase; phenylpropanoid pathway;
 KW isoflavone synthase; isoflavonoid biosynthesis; defence response;
 KW attractant; repellent; signal compound; antibiotic; transgenic plant;
 KW transgenic seed; PCR primer; ss.
 OS
 OS Glycine max.
 PN
 PN WO200044909-A1.
 XX
 PD 03-AUG-2000.
 XX
 PD 26-JAN-2000; 2000WO-US01772.
 PF
 PF 27-JAN-1999; 99US-0117769.
 PR
 PR 20-JUL-1999; 99US-0144783.
 PR
 PR 24-SEP-1999; 99US-0156094.
 XX
 XX (DUPO) DU PONT DE NEMOURS & CO E I.
 PA
 XX Fader GM, Jung W, McGonigle B, Odell JT, Yu X;

DR WPI; 2000-543395/49.
 XX Nucleic acids encoding isoflavonoid synthases, useful for producing
 PT transgenic plants with increased production of isoflavonoids which are
 PT involved in defense against phytopathogenic microorganisms -
 XX Example 14; Page 52; 157pp; English.
 PS
 XX Sequences AAA72437, AAA72449-A72461, AAA72468 and AAA72474-A72477
 CC represent cDNAs encoding novel plant isoflavone synthases (AAB21052 and
 CC AAB21054- AAB21071). Also disclosed is the soybean cytochrome P450
 CC monooxygenase CYP93C1, encoded by a known sequence (AAA72444, NCBI No.
 CC 2739005), which was identified in the present invention as having
 CC isoflavone synthase activity. The invention also relates to expression
 CC constructs, transformed host cells, and transgenic plants and seeds
 CC comprising the novel cDNA sequences of the invention. The invention also
 CC encompasses methods of altering isoflavone synthase expression in a host
 CC cell, altering isoflavonoid levels in a plant, and identifying nucleic
 CC acids encoding other plant isoflavone synthases. Isoflavone synthase
 CC plays a key role in the biosynthesis of isoflavonoids. Isoflavonoids are
 CC a class of secondary metabolites mainly produced in leguminous plants by
 CC a branch of the phenylpropanoid pathway. Isoflavone synthase catalyses
 CC the first step in the production of this pathway that commits metabolic
 CC intermediates to the synthesis of isoflavonoids. Isoflavonoids
 CC participate in the defence response of legumes against phytopathogenic
 CC microorganisms and are also involved in symbiotic relationships between
 CC the roots of legumes and rhizobial bacteria which eventually result in
 CC nodulation and nitrogen-fixation. They have also been shown to act as
 CC antibiotics, repellents, attractants, and signal compounds, and
 CC consumption of legume isoflavonoids is associated with health benefits
 CC in humans. The novel isoflavonoid synthases, and nucleic acids encoding
 CC them, are useful for altering the levels of isoflavonoids produced in
 CC legumes such as soybean, and for the production of isoflavonoids in
 CC plants which do not naturally produce them (e.g., maize, rice, wheat).
 CC Sequences AAA72478-A72481 represent PCR primers used in an
 CC exemplification of the invention to amplify DNA encoding soybean chalcone
 CC reductase (an enzyme that acts upstream of isoflavone synthase in the
 CC phenylpropanoid pathway).
 XX
 SQ Sequence 25 BP; 6 A; 7 C; 5 G; 7 T; 0 other;

Query Match 64.0%; Score 12.8; DB 21; Length 25;
 Best Local Similarity 87.5%; Pred. No. 1.1e+03;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 5 cccagggtgagtccttag 20
 ||||| ||||| |||||
 Db 17 CCCAGGTGAGTTTGAG 2

RESULT 8
 AAV00357/c
 ID AAV00357 standard; DNA; 29 BP.
 XX
 AC AAV00357;
 XX
 DT 23-APR-1998 (first entry)
 XX
 DE Bacillus thuringiensis insecticidal gene modification primer BTK58.
 XX
 KW Insecticidal protein; Bacillus thuringiensis; monocotyledonous plant;
 KW structural gene; maize; CryI(b); CryIIb; primer; ss.
 OS
 OS Synthetic.
 OS Bacillus thuringiensis.
 XX
 PN US5689052-A.
 PD
 PD 18-NOV-1997.
 XX
 PF 19-SEP-1995; 95US-0530492.
 XX

PR 22-DEC-1993; 93US-0172333.
XX 19-SEP-1995; 95US-0530492.
PA (MONS) MONSANTO CO.
XX Brown SM, Dean DA, Fromm ME, Sanders PR;
XX WPI; 1998-008070/01.
XX Genes encoding insecticidal proteins of *Bacillus thuringiensis* -
PT modified to enhance expression in monocotyledonous plants
XX Example 1; Column 17; 86pp; English.
XX The present sequence represents a primer used in the present invention
CC describing new structural genes capable of being expressed in a
CC monocotyledonous plant. The new genes comprise modified nucleotide
CC sequences which encode insecticidal proteins of *Bacillus thuringiensis*.
CC The genes have been modified to reduce the usage of codons that are
CC rare or semi-rare in monocotyledon DNA, thereby increasing
CC transformation efficiency and/or increasing accumulation of the
CC insecticidal protein in monocotyledon tissues.
XX Insecticidal protein in monocotyledon tissues.
XX Sequence 29 BP; 6 A; 9 C; 6 G; 8 T; 0 other;
SQ

Query Match 64.0%; Score 12.8; DB 19; Length 29;
Best Local Similarity 87.5%; Pred. No. 1.1e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 agtaccaggtagtc 16
||| ||||| |||||
DB 24 AGTCCCCAGGAGATC 9

RESULT 9
AAAF73275/c
ID AAF73275 standard; DNA; 29 BP.
XX
XX AAF73275;
XX
XX 26-APR-2001 (first entry)
XX
XX Oligonucleotide #66.
XX
XX CryIA; transgenic; crystal; toxin; insecticide; ss.
XX Synthetic.
XX
XX US6180774-B1.
XX
XX 30-JAN-2001.
XX
XX 05-AUG-1997; 97US-0906517.
XX
XX 19-SEP-1995; 95US-0530492.
XX 22-DEC-1993; 93US-0172333.
XX
XX (MONS) MONSANTO CO.
XX
XX Brown SM, Dean DA, Fromm ME, Sanders PR;
XX WPI; 2001-190861/19.
XX
XX Novel nucleic acids, useful for transgenic plant production which is
PT capable of expressing increased levels of desired proteins -
XX
XX Example 1; Column 16; 81pp; English.
XX
XX The present invention relates to nucleotides 669-1348 of a
CC *B.thuringiensis* CryIA(b). The invention is useful for transgenic
CC plant production, e.g. maize, capable of expressing increased
CC amount of transgenic protein, e.g. crystal protein toxin gene

CC of *Bacillus thuringiensis*.
XX Sequence 29 BP; 6 A; 9 C; 6 G; 8 T; 0 other;
SQ

Query Match 64.0%; Score 12.8; DB 22; Length 29;
Best Local Similarity 87.5%; Pred. No. 1.1e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 agtaccaggtagtc 16
||| ||||| |||||
DB 24 AGTCCCCAGGAGATC 9

RESULT 10
AAV15506
ID AAV15506 standard; DNA; 34 BP.
XX
XX AAV15506;
XX 11-JUN-1998 (first entry)
XX
XX Primer for adeno-associated virus DNA.
XX
XX AAV; vector; rep 68/78; PCR primer; gene therapy; ss.
XX Synthetic.
XX Adeno associated virus.
XX
XX WO9749824-A1.
XX 31-DEC-1997.
XX
XX 24-JUN-1997; 97WO-DE01333.
XX
XX 24-JUN-1996; 96DE-1025188.
XX
XX (MEDI-) MEDIGENE GMBH.
XX (MEDI-) MEDIGENE AG.
XX
XX Bogedain C, Hallek M, Maass G;
XX WPI; 1998-086641/08.
XX
XX System of adeno-associated viral vector and rep 68/78 sequence of
PT this virus- expression of which is delayed until replication of
PT viral DNA has started, provides large scale production of vectors
PT for gene therapy
XX
XX Example; Page 7; 20pp; German.
XX
XX The present sequence was used in the development of a novel system,
CC comprising an adeno-associated virus (AAV) vector containing a
CC foreign DNA, and the rep 68/78 sequence of AAV, the expression of
CC which is delayed. The components may be present in cis (in a single
CC agent) or in trans (in separate agents).
CC The system is used for production of AAV vectors, particularly for
CC gene therapy. The foreign DNA may encode a therapeutic protein, or
CC e.g. interferon, interleukin, growth factor, coagulation factor or
CC metabolic enzyme, particularly one that increases the
CC immunogenicity of tumour cells, and/or a diagnostic protein. The
CC system produces AAV vectors on a large scale. It is based on the
CC discovery that the rep68 and 78 proteins interfere with replication
CC of AAV DNA, and that this interference is overcome by delaying
CC expression of these proteins.
XX
XX Sequence 34 BP; 4 A; 13 C; 9 G; 8 T; 0 other;
SQ

Query Match 64.0%; Score 12.8; DB 19; Length 34;
Best Local Similarity 87.5%; Pred. No. 1.1e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 gtaccagtgagtct 17
 ||| ||| ||| |||
 Db 5 gtaccagtgagtct 20

RESULT 11
 AAV82665/C

ID AAV82665 standard; DNA; 48 BP.

XX AC AAV82665;

XX DT 25-FEB-1999 (first entry)

XX DE Target oligonucleotide JN5.

XX KW Detector oligonucleotide; hairpin structure; fluorescence;

XX KW primer extension; hybridization; signal primer; frameshift mutation;
 ss.

XX OS Synthetic.

XX PN EP881302-A2.

XX PD 02-DEC-1998.

XX PF 28-MAY-1998; 98EP-0109682.

XX PR 30-MAY-1997; 97US-0865675.

XX PA (BECT) BECTON DICKINSON & CO.

XX PI Linn PC, Nadeau JG, Pitner BJ, Schram JL;

XX DR WPI; 1999-001406/01.

XX PT New detector oligo:nucleotide having base-paired region carrying
 quenched dyes - where dyes become fluorescent when region is
 unpaired, useful for detection and amplification of target nucleic
 acid

XX PS Example 2; Page 12; 20pp; English.

CC Target oligonucleotides AAV82665-68 were designed to hybridize to the
 detector oligonucleotide of the invention. The detector oligonucleotide
 comprises a single-stranded target-binding region and an
 intramolecularly base-paired secondary structure linked to two dyes
 (donor and acceptor fluorophores). In the secondary structure,
 fluorescence of the donor is quenched, but when it is linearized or
 unfolded a change in some fluorescence parameter becomes detectable. A
 target nucleic acid is detected by hybridizing it to a detector
 oligonucleotide in which the secondary structure is 5' to the target
 binding region, primer extension to produce a complementary strand using
 the secondary structure as template, resulting in linearization or
 unfolding of it and detecting a change in fluorescence. The detector
 oligonucleotide are used to detect (by primer extension and
 hybridization) and amplify (as signal primer) target sequences, e.g. for
 detecting frameshift mutations.

XX SQ Sequence 48 BP; 15 A; 8 C; 10 G; 15 T; 0 other;

Query Match 64.0%; Score 12.8; DB 20; Length 48;

Best Local Similarity 87.5%; Pred. NO. 1.2e+03;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 taccagtgagtctt 18

||| ||| ||| |||

Db 41 TACTCAGATGAGTCTT 26

RESULT 12

ID AAV82663 standard; DNA; 20 BP.

XX AC AAF62963;

XX DT 08-MAY-2001 (first entry)

XX DE Mouse PEPCK-cytosolic antisense oligonucleotide ISIS 113360.

XX KW Mouse; antiinflammatory; cytostatic; antisense gene therapy;

XX KW phosphoenol pyruvate carboxykinase-cytosolic; PEPCK-cytosolic;

XX KW infection; Inflammation; tumour formation; phosphorothioate; ss.

XX OS Mus musculus.

XX PN US6187545-B1.

XX PD 13-FEB-2001.

XX PF 21-JAN-2000; 2000US-0488671.

XX PR 21-JAN-2000; 2000US-0488671.

XX PA (ISIS-) ISIS PHARM INC.

XX PI McKay R, Butler MM, Wyatt J, Cowdery LM;

XX DR WPI; 2001-190979/19.

XX PT Antisense compound capable of modulating the expression of phosphoenol
 pyruvate carboxykinase-cytosolic, useful for preventing or delaying
 infection, inflammation or tumor formation -

XX PS Example 17; Column 44; 64pp; English.

XX CC The present sequence is one of a number of antisense compounds of up to
 30 nucleobases in length that are capable of inhibiting the expression of
 phosphoenol pyruvate carboxykinase-cytosolic (PEPCK-cytosolic). The
 antisense compounds are useful for inhibiting the expression of
 PEPCK-cytosolic in cells or tissues. They are commonly used as research
 reagents and in diagnostics, e.g. to elucidate the function of particular
 genes. They are also useful for distinguishing between functions of
 various members of a biological pathway and for research use. The
 antisense compounds are also useful prophylactically, e.g. to prevent or
 delay infection, inflammation or tumour formation. The present sequence
 is a chimeric phosphorothioate oligonucleotide with 2'-MOE wings and a
 deoxy gap.

XX SQ Sequence 20 BP; 5 A; 6 C; 5 G; 4 T; 0 other;

Query Match 62.0%; Score 12.4; DB 22; Length 20;

Best Local Similarity 92.9%; Pred. NO. 1.8e+03;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 cccagtgagtctt 18

||| ||| ||| |||

Db 15 CCAAGGTGAGTCTT 2

RESULT 13

ID AAQ82668/C

XX ID AAQ82668 standard; DNA; 22 BP.

XX AC AAQ82668;

XX DT 14-SEP-1995 (first entry)

XX DE Chromosome 11 (locus LDHC) STS primer LDHC-Z.

XX KW sequence sampled mapping; genomic analysis; complex genome mapping;
 cosmid library; chromosome 11; sequence tagged site; STS analysis; ss.

XX OS Synthetic.

PN WO9429486-A.
 XX
 PD 22-DEC-1994.
 XX
 PF 15-JUN-1994; 94WO-US06810.
 XX
 XX 15-JUN-1993; 93US-0078471.
 PR 07-SEP-1993; 93US-0117952.
 XX
 XX (SALK) SALK INST BIOLOGICAL STUDIES.
 PA
 XX Evans GA, Smith MW;
 PI
 XX WPI; 1995-036508/05.
 DR
 XX

XX Sequencing complex genomes, present as fragments in a cosmid
 PT library - by sequencing end-specific nucleotides of each clone
 PT then correlating with spatial relationship of cosmid, esp. for
 PT mammalian chromosomes.
 XX

XX Example 4; Page 92; 128pp; English.

XX Sequences were determined from the ends of chromosome 11-specific
 CC cosmid by automated sequencing without intermediate subcloning.
 CC A sample of 371 DNA sequence fragments were determined and of
 CC these, 277 were suitable for STS primer prediction by computer
 CC analysis (using the "primer" program available from E.Lander, MIT).
 CC The STSS and cosmid were mapped by in situ hybridisation, somatic
 CC cell hybrid analysis or both. Using this method, 370 STSS specific
 CC for human chromosome 11 were generated and most of them were
 CC regionally mapped. This procedure illustrates a novel method for
 CC sequencing complex genomes, designated "sequence sampled mapping".
 CC The sequence sampled mapping method is useful for the completion of
 CC high density sequence-based maps, and ultimately, for the complete
 CC sequencing of genomic DNA directly from cosmid clones.
 CC See AAQ82001-Q82706 and AAQ91325-Q91358 for STS primers.
 XX

SQ Sequence 22 BP; 8 A; 5 C; 4 G; 5 T; 0 other;

Query Match 62.0%; Score 12.4; DB 16; Length 22;
 Best Local Similarity 92.9%; Pred. No. 1.8e+03;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 acccaggtgagtct 17
 DB 14 ATCCAGGTGAGTCT 1

RESULT 14
 AAQ86221
 ID AAQ86221 standard; DNA; 33 BP.
 XX
 AC AAQ86221;

DT 12-DEC-1995 (first entry)
 XX
 DE GC PCR primer #2.
 XX

KW Eukaryotic layered vector initiation system; Sindbis; alphavirus; PCR;
 KW transcription initiation; non-structural protein; subgenomic fragment;
 KW RNA polymerase recognition sequence; ELVIS; gene therapy; amplify;
 KW primer; polymerase chain reaction; cystic fibrosis;
 KW glucocerebrosidase; ss.

OS Synthetic.

XX WO9507994-A.

XX 23-MAR-1995.

PF 15-SEP-1994; 94WO-US10469.

XX

PR 15-SEP-1993; 93US-0122791.
 PR 18-FEB-1994; 94US-0198450.
 XX
 PA (VIAG-) VIAGENE INC.
 XX
 PI Chang SMW, Driver DA, Dubensky TW, Ibanez CE, Jolly DJ;
 PI POLO JM;
 XX
 DR WPI; 1995-131362/17.
 XX
 XX New alpha virus vectors for gene therapy - of viral infection,
 PT cancer, auto-immune disease, etc., and as vaccines.
 PT
 XX Example 13; Page 154; 260pp; English.

XX The sequences given in AAQ86220-21 are primers which were used in the
 CC construction of a Sindbis glucocerebrosidase (GC) vector producing
 CC cell line. These primers amplify a 521 bp fragment for GC screening
 CC of the transformant cell lines. The cell lines contain alphavirus
 CC vectors which express multiple heterologous genes. The vectors are
 CC eukaryotic layered vector initiation systems (ELVIS) derived from
 CC Sindbis. ELVIS's comprise a 5' sequence capable of initiating
 CC transcription of an alphavirus, a nucleotide sequence encoding
 CC alphavirus non-structural proteins, a viral junction region which
 CC has been inactivated such that viral transcription of the subgenomic
 CC fragment is prevented, and an alphavirus RNA polymerase recognition
 CC sequence. Inactivation of the viral junction region prevents
 CC transcription of the subgenomic fragment making vectors such as this
 CC suitable for a wide variety of applications, eg. gene therapy for the
 CC treatment of cystic fibrosis.
 XX

SQ Sequence 33 BP; 10 A; 5 C; 11 G; 7 T; 0 other;

Query Match 62.0%; Score 12.4; DB 16; Length 33;
 Best Local Similarity 92.9%; Pred. No. 1.8e+03;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 agtaccaggtgag 14
 DB 6 agtagccaggcgag 19

RESULT 15
 AAQ86223
 ID AAQ86223 standard; DNA; 33 BP.
 XX
 AC AAQ86223;

DT 12-DEC-1995 (first entry)
 XX
 DE GC PCR (R) primer #2.
 XX

KW Eukaryotic layered vector initiation system; Sindbis; alphavirus; PCR;
 KW transcription initiation; non-structural protein; subgenomic fragment;
 KW RNA polymerase recognition sequence; ELVIS; gene therapy; amplify;
 KW primer; polymerase chain reaction; cystic fibrosis;
 KW glucocerebrosidase; ss.

OS Synthetic.

XX WO9507994-A.

XX 23-MAR-1995.

PF 15-SEP-1994; 94WO-US10469.

XX 15-SEP-1993; 93US-0122791.

XX 18-FEB-1994; 94US-0198450.

XX (VIAG-) VIAGENE INC.

PI Chang SMW, Driver DA, Dubensky TW, Ibanez CE, Jolly DJ;

```
PI Polo JM;
XX
DR WPI; 1995-131362/17.
XX
XX
PT New alpha virus vectors for gene therapy - of viral infection,
PT cancer, auto-immune disease, etc., and as vaccines.
XX
XX
PS Example 17; Page 166; 260pp; English.
XX
XX
CC The sequences given in AA086222-23 are primers which were used in the
CC construction of a Sindbis glucocerebrosidase (GC) vector producing
CC cell line. These primers amplify a 521 bp fragment for GC screening
CC of the transformant cell lines. The cell lines contain alphavirus
CC vectors which express multiple heterologous genes. The vectors are
CC eukaryotic layered vector initiation systems (ELVIS) derived from
CC Sindbis. ELVIS's comprise a 5' sequence capable of initiating
CC transcription of an alphavirus, a nucleotide sequence encoding
CC alphavirus non-structural proteins, a viral junction region which
CC has been inactivated such that viral transcription of the subgenomic
CC fragment is prevented, and an alphavirus RNA polymerase recognition
CC sequence. Inactivation of the viral junction region prevents
CC transcription of the subgenomic fragment making vectors such as this
CC suitable for a wide variety of applications, eg. gene therapy for the
CC treatment of cystic fibrosis.
XX
SQ Sequence 33 BP; 10 A; 5 C; 11 G; 7 T; 0 other;

Query Match 62.0%; Score 12.4; DB 16; Length 33;
Best Local Similarity 92.9%; Pred.No. 1.8e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 agtaccagggtgag 14
   ||| |||||
Db 6 agtagccagggtgag 19

Search completed: October 2, 2001, 16:18:40
Job time: 15484 sec
```

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 2, 2001, 16:03:48 ; Search time 417.38 Seconds
(without alignments)
9.071 Million cell updates/sec

Title: US-09-757-100B-10

Perfect score: 20

Sequence: 1 ggtaagcagctgccattatt 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 324599 seqs, 9465562 residues

Total number of hits satisfying chosen parameters: 460742

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_NA:*

- 1: /cgn2.6/ptodata/1/ina/5A_COMB.seq:*
- 2: /cgn2.6/ptodata/1/ina/5B_COMB.seq:*
- 3: /cgn2.6/ptodata/1/ina/6A_COMB.seq:*
- 4: /cgn2.6/ptodata/1/ina/6B_COMB.seq:*
- 5: /cgn2.6/ptodata/1/ina/PTUS_COMB.seq:*
- 6: /cgn2.6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	3	US-09-377-310-10
2	15	75.0	15	3	US-09-377-310-30
3	13.8	69.0	30	2	US-08-471-371-6
4	13.6	68.0	30	2	US-08-833-377-5
5	13.4	67.0	18	1	US-08-378-761A-45
6	13.4	67.0	18	1	US-08-485-286-45
7	13.2	66.0	30	1	US-07-985-691-6
8	12.6	63.0	29	3	US-09-106-216-52
9	12.6	63.0	44	4	US-09-042-353-374
10	12.6	63.0	49	3	US-09-106-216-53
11	12.4	62.0	39	2	US-08-484-397A-24
12	12.2	61.0	25	1	US-08-482-115B-26
13	12.2	61.0	25	1	US-08-752-929-22
14	12.2	61.0	25	2	US-08-472-802C-27
15	12.2	61.0	41	5	PCT-US96-09455A-186
16	12.2	61.0	49	3	US-08-617-454-9
17	12.2	61.0	49	2	US-09-157-206-5
18	12.2	61.0	49	4	US-09-447-863-5
19	12.2	61.0	49	5	PCT-US96-09455A-185
20	12	60.0	29	3	US-08-826-964-4
21	12	60.0	39	2	US-08-951-822-13
22	12	60.0	39	4	US-09-173-043-28
23	12	60.0	42	2	US-08-436-664-3
24	12	60.0	42	2	US-08-436-664-4
25	12	60.0	42	3	US-09-135-642-3
26	12	60.0	42	3	US-09-135-642-4
27	12	60.0	42	3	US-08-394-232A-3

ALIGNMENTS

RESULT 1

US-09-377-310-10

; Sequence 10, Application US/09377310B

; Patent No. 6133031

; GENERAL INFORMATION:

; APPLICANT: Monia, Brett P.

; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase

; FILE REFERENCE: ISPH-0389

; CURRENT APPLICATION NUMBER: US/09/377,310B

; CURRENT FILING DATE: 1999-08-19

; NUMBER OF SEQ ID NOS: 43

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 10

; LENGTH: 20

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: antisense sequence

US-09-377-310-10

Query Match 100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ggtaagcagctgccattatt 20

Db 1 ggtaagcagctgccattatt 20

RESULT 2

US-09-377-310-30

; Sequence 30, Application US/09377310B

; Patent No. 6133031

; GENERAL INFORMATION:

; APPLICANT: Monia, Brett P.

; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase

; FILE REFERENCE: ISPH-0389

; CURRENT APPLICATION NUMBER: US/09/377,310B

; CURRENT FILING DATE: 1999-08-19

; NUMBER OF SEQ ID NOS: 43

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 30

; LENGTH: 15

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:
; OTHER INFORMATION: antisense sequence
US-09-377-310-30

Query Match 75.0%; Score 15; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 3 taagcagctgccatt 17
|||||
Db 1 taagcagctgccatt 15

RESULT 3
US-08-471-371-6
; Sequence 6, Application US/08471371
; Patent No. 5981215
; GENERAL INFORMATION:
; APPLICANT: Meissner, Paul S.
; APPLICANT: Coleman, Timothy A.
; TITLE OF INVENTION: HUMAN CRIPTIN GROWTH FACTOR
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
; ADDRESSEE: STEWART & OLSTEIN
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: N.J.
; COUNTRY: U.S.A.
; ZIP: 07068

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471.371
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:
; NAME: Ferraro, Gregory D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 32580-455
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (201) 994-1700
; TELEFAX: (201) 994-1744
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "PRIMER"
US-08-471-371-6

Query Match 69.0%; Score 13.8; DB 2; Length 30;
Best Local Similarity 88.2%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 4 aagcagctgccatt 20
|||||
Db 4 AACGAGCTGCTATTATT 20

RESULT 4
US-08-833-377-5
; Sequence 5, Application US/08833377
; Patent No. 5968506
; GENERAL INFORMATION:
; APPLICANT: Weirich, Scott L.

; APPLICANT: Atkinson III, Edward M.
; APPLICANT: Lichtsteiner, Serge P.
; APPLICANT: Vasserot, Alain P.
; APPLICANT: Pruzan, Ronald A.
; APPLICANT: Kealey, James T.
; TITLE OF INVENTION: Purified Telomerase
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/833.377
; FILING DATE: 04-APR-1997
; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/510,736
; FILING DATE: 04-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-001110US

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:

; NAME/KEY: modified_base
; LOCATION: 1
; OTHER INFORMATION: /mod_base= OTHER
; OTHER INFORMATION: /note= "N = 5' biotinylated guanosine"
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..30
; OTHER INFORMATION: /note= "Oligo 13"
US-08-833-377-5

Query Match 68.0%; Score 13.6; DB 2; Length 30;
Best Local Similarity 80.0%; Pred. No. 2.1e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1 ggtaagcagctgccatt 20
|||||
Db 6 GGCCAGCAGCTGCATTTT 25

RESULT 5
US-08-378-761A-45/c
; Sequence 45, Application US/08378761A
; Patent No. 5635384
; GENERAL INFORMATION:
; APPLICANT: WALSH, TERENCE A
; APPLICANT: HEY, TIMOTHY D
; APPLICANT: MORGAN, ALICE ER
; TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
; TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
; TITLE OF INVENTION: USING
; NUMBER OF SEQUENCES: 81

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: ANDREA T. BORUCKI
;; STREET: 9330 ZIONSVILLE ROAD
;; CITY: INDIANAPOLIS
;; STATE: IN
;; COUNTRY: US
;; ZIP: 46268
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/378,761A
;; FILING DATE: 26-JAN-1995
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: BORUCKI, ANDREA T
;; REGISTRATION NUMBER: 33651
;; REFERENCE/DOCKET NUMBER: 38272B
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (317) 337-4846
;; INFORMATION FOR SEQ ID NO: 45:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 18 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; US-08-378-761A-45

Query Match 67.0%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 2.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 taagcagctgccatt 17
|||||
Db 17 TAAGCAGCTGCAATT 3

RESULT 6
US-08-485-286-45/c
;; Sequence 45, Application US/08485286
;; Patent No. 5646026
;; Patent No. 5646026 5646119
;; GENERAL INFORMATION:
;; APPLICANT: WALSH, TERENCE A
;; APPLICANT: HEY, TIMOTHY D
;; APPLICANT: MORGAN, ALICE ER
;; TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
;; TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
;; TITLE OF INVENTION: USING
;; NUMBER OF SEQUENCES: 81
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: ANDREA T. BORUCKI
;; STREET: 9330 ZIONSVILLE ROAD
;; CITY: INDIANAPOLIS
;; STATE: IN
;; COUNTRY: US
;; ZIP: 46268
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/485,286
;; FILING DATE:
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/378761
;; FILING DATE: 26-JAN-1995
;; ATTORNEY/AGENT INFORMATION:

;; NAME: BORUCKI, ANDREA T
;; REGISTRATION NUMBER: 33651
;; REFERENCE/DOCKET NUMBER: 38272B
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (317) 337-4846
;; INFORMATION FOR SEQ ID NO: 45:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 18 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; US-08-485-286-45

Query Match 67.0%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 2.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 taagcagctgccatt 17
|||||
Db 17 TAAGCAGCTGCAATT 3

RESULT 7
US-07-985-691-6/c
;; Sequence 6, Application US/07985691
;; Patent No. 5405946
;; GENERAL INFORMATION:
;; APPLICANT: Griffin, John H
;; APPLICANT: Bouma, Bonno N
;; APPLICANT: Bertina, Rogier
;; TITLE OF INVENTION: RECOMBINANT PROTEIN S VARIANTS DEFICIENT
;; TITLE OF INVENTION: IN C4BP BINDING ACTIVITY, COMPOSITIONS AND THERAPEUTIC
;; TITLE OF INVENTION: METHODS
;; NUMBER OF SEQUENCES: 17
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: The Scripps Research Institute, Office of
;; ADDRESSEE: Patent Counsel
;; STREET: 10666 No. 5405946th Torrey Pines Road, TPC 8
;; CITY: La Jolla
;; STATE: CA
;; COUNTRY: USA
;; ZIP: 92037
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/07/985,691
;; FILING DATE: 19921202
;; CLASSIFICATION: 514
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Fitting, Thomas
;; REGISTRATION NUMBER: 34,163
;; REFERENCE/DOCKET NUMBER: TSR0042P
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 619-554-2937
;; TELEFAX: 619-554-6312
;; INFORMATION FOR SEQ ID NO: 6:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 30 base pairs
;; TYPE: NUCLEIC ACID
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; US-07-985-691-6

Query Match 66.0%; Score 13.2; DB 1; Length 30;
Best Local Similarity 83.3%; Pred. No. 3.3e+02;

; FILING DATE: 01-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 014643-009040US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 374:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 44 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-09-042-353-374

Query Match 63.0%; Score 12.6; DB 4; Length 44;
Best Local Similarity 78.9%; Pred. No. 7e+02;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ggtaagcagctgctattat 19
Db 26 GCTAACCAGCTGCTAATAT 8

RESULT 10

US-09-106-216-53/c
; Sequence 53, Application US/09106216
; Patent No. 6153386
; GENERAL INFORMATION:
; APPLICANT: Lalouel, Jean-Marie
; APPLICANT: Jeunemaitre, Xavier
; APPLICANT: Lofton, Richard P.
; APPLICANT: Soubrier, Florent
; APPLICANT: Kotelevtsev, Yuri
; APPLICANT: Corvol, Pierre
; TITLE OF INVENTION: Method to Determine Predisposition to
; TITLE OF INVENTION: Hypertension
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rothwell, Figg, Ernst & Kurz
; STREET: 555 Thirteenth Street N.W., Suite 701-E
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/106,216
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/
; FILING DATE: 08-JUN-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/319,545
; FILING DATE: 07-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/952,545
; FILING DATE: 30-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Ihnen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 2323-124
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-783-6040
; TELEFAX: 202-783-6031

; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 49 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "primer"
US-09-106-216-53

Query Match 63.0%; Score 12.6; DB 3; Length 49;
Best Local Similarity 78.9%; Pred. No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 gtaagcagctgctattatt 20
Db 46 GGAAGAAGCTCCCGTGT 28

RESULT 11

US-08-484-397A-24/c
; Sequence 24, Application US/08484397A
; Patent No. 5869055
; GENERAL INFORMATION:
; APPLICANT: Juan, Shao-Chieh
; APPLICANT: Lichenstein, Henri S.
; APPLICANT: Wright, Samuel D.
; TITLE OF INVENTION: ANTI-INFLAMMATORY CD14 POLYPEPTIDES
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: AMGEN INC
; STREET: 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: CA
; COUNTRY: US
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,397A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Curry, Daniel R.
; REGISTRATION NUMBER: 32,727
; REFERENCE/DOCKET NUMBER: A-324A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 805/447-1000
; TELEFAX: 805/447-1090
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-08-484-397A-24

Query Match 62.0%; Score 12.4; DB 2; Length 39;
Best Local Similarity 92.9%; Pred. No. 8.7e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 agcagctgcccatta 18
Db 24 AGCAGCTGCCCTTTA 11

RESULT 12

US-08-482-115B-26
; Sequence 26, Application US/08482115B
; Patent No. 5776679
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Assays for the RNA Component of Human
; TITLE OF INVENTION: Telomerase
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,115B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-000830US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-482-115B-26

Query Match 61.0%; Score 12.2; DB 1; Length 25;
Best Local Similarity 82.4%; Pred. No. le+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 gtaagcagctgccatt 17
|| ||||| |||||
Db 9 GGCCAGCAGCTGACATT 25

RESULT 13
US-08-752-929-22
; Sequence 22, Application US/08752929
; Patent No. 5798259
; GENERAL INFORMATION:
; APPLICANT: YAZAWA, Kazunaga
; APPLICANT: YAMADA, Akiko
; APPLICANT: KATO, Seishi
; APPLICANT: KONDO, Kiyosi
; TITLE OF INVENTION: Gene Coding for Eicosapentaenoic Acid Synthesizing
; TITLE OF INVENTION: Enzymes and Process for Production of Eicosapentaenoic
; TITLE OF INVENTION: Acid
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/752,929
; FILING DATE: 20-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/375,709
; FILING DATE: 20-JAN-1995
; PRIOR APPLICATION NUMBER: US 08/178,251
; FILING DATE: 14-MAY-1993
; APPLICATION NUMBER: JP 4-147945
; FILING DATE: 15-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: WEGNER, Harold C.
; REGISTRATION NUMBER: 25,258
; REFERENCE/DOCKET NUMBER: 53466/150/AAOK
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-752-929-22

Query Match 61.0%; Score 12.2; DB 1; Length 25;
Best Local Similarity 82.4%; Pred. No. le+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 taagcagctgccatt 19
| | | | | | | | | |
Db 5 TCATCAGGTGCCATTAT 21

RESULT 14
US-08-472-802C-27
; Sequence 27, Application US/08472802C
; Patent No. 5958680
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/472,802C
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15389-000820
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-472-802C-27

Query Match 61.0%; Score 12.2; DB 2; Length 25;
Best Local Similarity 82.4%; Pred. No. 1e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ggtaagcagctgccatt 17
||| ||||| |||||
Db 9 GCCCAGCAGCTGACATT 25

RESULT 15

PCT-US96-09455A-186/c
Sequence 186, Application PC/TUS9609455A
GENERAL INFORMATION:
APPLICANT: PARMA, et al.
TITLE OF INVENTION: HIGH AFFINITY NUCLEIC ACID
LIGANDS TO LECTINS
NUMBER OF SEQUENCES: 390
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MB
COMPUTER: IBM pc compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/09455A
FILING DATE: 05 JUNE 1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/479,724
FILING DATE: 07-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/472,256
FILING DATE: 07-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/472,255
FILING DATE: 07-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/477,829
FILING DATE: 07-JUNE-1995
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson

REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX40C/PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 186:
SEQUENCE CHARACTERISTICS:
LENGTH: 41 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
PCT-US96-09455A-186

Query Match 61.0%; Score 12.2; DB 5; Length 41;
Best Local Similarity 82.4%; Pred. No. 1.1e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 2 gtaagcagctgccatta 18
||||| | |||||
Db 41 GTAAGCCGAGGCCATTA 25

Search completed: October 2, 2001, 16:03:49
Job time: 14593 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: October 2, 2001, 16:55:07 ; Search time 2173.58 Seconds
(without alignments)
14.467 Million cell updates/sec

Title: US-09-757-100B-33
Perfect score: 15
Sequence: 1 tggctattcttcagt 15

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1895189 seqs, 1048201267 residues

Total number of hits satisfying chosen parameters: 299022

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_NA_New.*

- 1: /cgn2.6/ptodata/2/pna/PCT_NEW_COMB.seq.*
- 2: /cgn2.6/ptodata/2/pna/US06_NEW_COMB.seq.*
- 3: /cgn2.6/ptodata/2/pna/US07_NEW_COMB.seq.*
- 4: /cgn2.6/ptodata/2/pna/US08_NEW_COMB.seq.*
- 5: /cgn2.6/ptodata/2/pna/US09_NEW_COMB.seq.*
- 6: /cgn2.6/ptodata/2/pna/US09_NEW_COMB.seq.*
- 7: /cgn2.6/ptodata/2/pna/US09_NEW_COMB.seq.*
- 8: /cgn2.6/ptodata/2/pna/US60_NEW_COMB.seq.*

pred, No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
1	12.4	82.7	20	6	US-09-198-452A-3994
2	11.8	78.7	21	7	US-09-849-243-7
3	11.8	78.7	24	5	US-09-815-980-1
4	11.4	76.0	31	5	US-09-536-784-272
5	11.4	76.0	31	6	US-09-765-272-272
6	11	73.3	24	7	US-09-717-438-14
7	11	73.3	38	7	US-09-724-750-14025
8	11	73.3	39	7	US-09-724-750-24046
9	11	73.3	41	7	US-09-717-438-13
10	10.8	72.0	17	7	US-09-818-875-1707
11	10.8	72.0	17	7	US-09-818-875-1708
12	10.8	72.0	20	6	US-09-743-237-16
13	10.8	72.0	20	6	US-09-198-452A-1913
14	10.8	72.0	21	7	US-09-520-313-140
15	10.8	72.0	23	7	US-09-379-888B-8
16	10.8	72.0	31	5	US-09-700-492-3
17	10.4	69.3	17	5	US-09-708-690-9178
18	10.4	69.3	17	5	US-09-708-690-9179
19	10.4	69.3	17	6	US-09-866-108-1237
20	10.4	69.3	17	6	US-09-866-108-1238
21	10.4	69.3	17	6	US-09-866-108-1239
22	10.4	69.3	17	6	US-09-866-108-1240
23	10.4	69.3	17	6	US-09-866-108-1241
24	10.4	69.3	17	6	US-09-866-108-1242
25	10.4	69.3	17	6	US-09-866-108-2547

ALIGNMENTS

RESULT 1
US-09-198-452A-3994
; Sequence 3994, Application US/09198452A
; GENERAL INFORMATION:
; APPLICANT: Griffiths, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention and treatment of infection
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 3994
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-3994

Query Match 82.7%; Score 12.4; DB 6; Length 20;
Best Local Similarity 92.9%; Pred. No. 1.1e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ggcttattcttcagt 15
|||||
Db 1 ggcttattcttcagt 14

RESULT 2
US-09-849-243-7/c
; Sequence 7, Application US/09849243
; GENERAL INFORMATION:
; APPLICANT: Kirschbaum, Bernd
; Berglund, Erick
; Meisterernst, Michael
; Polites, Greg
TITLE OF INVENTION: PURIFICATION OF HIGHER ORDER TRANSCRIPTION COMPLEXES FROM TRANSGENIC NON-HUMAN ANIMALS
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: HELLER, EHRMAN, WHITE & MCAULIFFE
STREET: 1666 K Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20006
COMPUTER READABLE FORM:

Sequence 2548, Ap
Sequence 2549, Ap
Sequence 2550, Ap
Sequence 2551, Ap
Sequence 2552, Ap
Sequence 16, Appl
Sequence 19, Appl
Sequence 4166, Ap
Sequence 4167, Ap
Sequence 4168, Ap
Sequence 4169, Ap
Sequence 4170, Ap
Sequence 4171, Ap
Sequence 4172, Ap
Sequence 4173, Ap
Sequence 4174, Ap
Sequence 4175, Ap
Sequence 4176, Ap
Sequence 4177, Ap

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;
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/849,243
; FILING DATE: 07-May-2001
; ATTORNEY/AGENT INFORMATION:
; NAME: Granados, Patricia D.
; REGISTRATION NUMBER: 33,683
; REFERENCE/DOCKET NUMBER: 38005-0148
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)912-2000
; TELEFAX: (202)912-2020
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: exon
; LOCATION: 1..21
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-849-243-7

Query Match 78.7%; Score 11.8; DB 7; Length 21;
Best Local Similarity 86.7%; Pred. No. 2.5e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tggcttatcttcag 15
    ||||| || |||||
Db 19 TGGCCTAACTTCAGT 5

RESULT 3
US-09-815-980-1/c
; Sequence 1, Application US/09815980
; GENERAL INFORMATION:
; APPLICANT: Leiden, Jeffrey M.
; TITLE OF INVENTION: AN INDUCIBLE EUKARYOTIC EXPRESSION
; FILE REFERENCE: HUI-042
; CURRENT APPLICATION NUMBER: US/09/815,980
; CURRENT FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: US 60/191,568
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-815-980-1

Query Match 78.7%; Score 11.8; DB 5; Length 24;
Best Local Similarity 86.7%; Pred. No. 2.6e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tggcttatcttcag 15
    ||||| || |||||
Db 18 TGGCCTAACTTCAGT 4

RESULT 4
US-09-536-784-272
; Sequence 272, Application US/09536784
; GENERAL INFORMATION:
; APPLICANT: Choi et. al.
```

```
;
; TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
; NUMBER OF SEQUENCES: 452
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/536,784
; FILING DATE: 30-Oct-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/961,083
; FILING DATE: OCT-30-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Michelle S. Marks
; REGISTRATION NUMBER: 41,971
; REFERENCE/DOCKET NUMBER: PB340P3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 272:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 272:
US-09-536-784-272

Query Match 76.0%; Score 11.4; DB 5; Length 31;
Best Local Similarity 92.3%; Pred. No. 4.6e+03;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 gcttatcttcag 15
    ||||| |||||
Db 7 GCTTATCTGCAGT 19

RESULT 5
US-09-765-272-272
; Sequence 272, Application US/09765272
; GENERAL INFORMATION:
; APPLICANT: Choi et. al.
; TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
; NUMBER OF SEQUENCES: 452
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/765,272
; FILING DATE: 22-Jan-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/961,083
; FILING DATE: <Unknown>
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;
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB340P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 272:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 272:
US-09-765-272-272

Query Match 76.0%; Score 11.4; DB 6; Length 31;
Best Local Similarity 92.3%; Pred. No. 4.6e+03;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 gcttatcttcagt 15
Db 7 GCATTCTGCAGT 19

RESULT 6
US-09-717-438-14
; Sequence 14, Application US/09717438
; GENERAL INFORMATION:
; APPLICANT: Stemmer, Willem P.C.
; Cramer, Andreas M.
; TITLE OF INVENTION: Methods for Generating Polynucleotides
; Having Desired Characteristics by Iterative Selection and
; Recombination
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/717,438
; FILING DATE: 18-Nov-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/621,859
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/537,874
; FILING DATE: 30-OCT-1995
; APPLICATION NUMBER: WO PCT/US95/02126
; FILING DATE: 17-FEB-1995
; APPLICATION NUMBER: US 08/198,431
; FILING DATE: 17-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Liebeschuetz, Joe
; REGISTRATION NUMBER: 37,505
; REFERENCE/DOCKET NUMBER: 018097-014612US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
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```
;
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-717-438-14

Query Match 73.3%; Score 11; DB 7; Length 24;
Best Local Similarity 100.0%; Pred. No. 7.4e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 cttatcttcag 14
Db 2 CTTATCTTCAG 12

RESULT 7
US-09-724-750-14025
; Sequence 14025, Application US/09724750
; GENERAL INFORMATION:
; APPLICANT: Havukkala, Ilkka
; TITLE OF INVENTION: Polynucleotide, Materials Incorporating
; FILE REFERENCE: 11000.1049AU
; CURRENT APPLICATION NUMBER: US/09/724,750
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/171,431
; PRIOR FILING DATE: 1999-12-21
; NUMBER OF SEQ ID NOS: 25199
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14025
; LENGTH: 38
; TYPE: DNA
; ORGANISM: Pinus radiata
US-09-724-750-14025

Query Match 73.3%; Score 11; DB 7; Length 38;
Best Local Similarity 100.0%; Pred. No. 8e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ggcttatcttc 12
Db 27 ggcttatcttc 37

RESULT 8
US-09-724-750-24046
; Sequence 24046, Application US/09724750
; GENERAL INFORMATION:
; APPLICANT: Havukkala, Ilkka
; TITLE OF INVENTION: Polynucleotide, Materials Incorporating
; FILE REFERENCE: 11000.1049AU
; CURRENT APPLICATION NUMBER: US/09/724,750
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/171,431
; PRIOR FILING DATE: 1999-12-21
; NUMBER OF SEQ ID NOS: 25199
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24046
; LENGTH: 39
; TYPE: DNA
; ORGANISM: Pinus radiata
US-09-724-750-24046

Query Match 73.3%; Score 11; DB 7; Length 39;
Best Local Similarity 100.0%; Pred. No. 8.1e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ggcttatcttc 12
Db 23 ggcttatcttc 33
```

RESULT 9
US-09-717-438-13/c
; Sequence 13, Application US/09717438
; GENERAL INFORMATION:
; APPLICANT: Stemmer, Willem P.C.
; Cramer, Andreas M.
; TITLE OF INVENTION: Methods for Generating Polynucleotides
; Having Desired Characteristics by Iterative Selection and
; Recombination
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/09/717,438
; FILING DATE: 18-Nov-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/621,859
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/537,874
; FILING DATE: 30-OCT-1995
; APPLICATION NUMBER: WO PCT/US95/02126
; FILING DATE: 17-FEB-1995
; APPLICATION NUMBER: US 08/198,431
; FILING DATE: 17-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Liebeschuetz, Joe
; REGISTRATION NUMBER: 37,505
; REFERENCE/DOCKET NUMBER: 018097-01461205
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 41 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-717-438-13

Query Match 73.3%; Score 11; DB 7; Length 41;
Best Local Similarity 100.0%; Pred. No. 8.1e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 cttatcttcag 14
| | | | | | | | | |
Db 22 CTTATCTTCAG 12

RESULT 10
US-09-818-875-1707
; Sequence 1707, Application US/09818875
; GENERAL INFORMATION:
; APPLICANT: Kmiec, Eric B.
; APPLICANT: Gampfer, Howard B.
; APPLICANT: Rice, Michael C.
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single
; TITLE OF INVENTION: Stranded Oligonucleotides

; FILE REFERENCE: Napro-4
; CURRENT APPLICATION NUMBER: US/09/818,875
; CURRENT FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 60/192,176
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/192,179
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/208,538
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/244,989
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 4385
; SOFTWARE: Friedman macro Napro4
; SEQ ID NO 1707
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-818-875-1707

Query Match 72.0%; Score 10.8; DB 7; Length 17;
Best Local Similarity 85.7%; Pred. No. 9.2e+03;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tggcttatcttcag 14
| | | | | | | | | |
Db 4 tagtttatcttcag 17

RESULT 11
US-09-818-875-1708/c
; Sequence 1708, Application US/09818875
; GENERAL INFORMATION:
; APPLICANT: Kmiec, Eric B.
; APPLICANT: Gampfer, Howard B.
; APPLICANT: Rice, Michael C.
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single
; TITLE OF INVENTION: Stranded Oligonucleotides
; FILE REFERENCE: Napro-4
; CURRENT APPLICATION NUMBER: US/09/818,875
; CURRENT FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 60/192,176
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/192,179
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/208,538
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/244,989
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 4385
; SOFTWARE: Friedman macro Napro4
; SEQ ID NO 1708
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-818-875-1708

Query Match 72.0%; Score 10.8; DB 7; Length 17;
Best Local Similarity 85.7%; Pred. No. 9.2e+03;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tggcttatcttcag 14
| | | | | | | | | |
Db 14 TAGTTTATCTTCAG 1

RESULT 12
US-09-743-237-16/c
; Sequence 16, Application US/09743237
; GENERAL INFORMATION:
; APPLICANT: SUGIHARA, TAKASHI
; APPLICANT: WADHWA, RENU

; APPLICANT: KAUL, SUNIL C.
; APPLICANT: MITSUI, YUJI
; TITLE OF INVENTION: TESTIS-SPECIFIC DIFFERENTIATION-REGULATORY FACTOR
; FILE REFERENCE: 084335/0127
; CURRENT APPLICATION NUMBER: US/09/743,237
; CURRENT FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: PCT/JP99/03859
; PRIOR FILING DATE: 1999-07-16
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-743-237-16

Query Match 72.0%; Score 10.8; DB 6; Length 20;
Best Local Similarity 85.7%; Pred. No. 9.4e+03;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ggcttattcttcagt 15
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Db 19 GGCTTGCTTGAGT 6

RESULT 13
US-09-198-452A-1913/c
; Sequence 1913, Application US/09198452A
; GENERAL INFORMATION:
; APPLICANT: Griffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 1913
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-1913

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Best Local Similarity 85.7%; Pred. No. 9.4e+03;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tggcttattcttcag 14
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Db 15 TGGATTAACTTCAG 2

RESULT 14
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; Sequence 140, Application US/09920313
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; TITLE OF INVENTION: Nucleic Acids for the Prevention and
; TITLE OF INVENTION: Treatment of Gastric Ulcers
; FILE REFERENCE: C1037/7019 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/920,313
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: US 60/222,248
; PRIOR FILING DATE: 2001-08-08
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 140
; LENGTH: 21

; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-920-313-140

Query Match 72.0%; Score 10.8; DB 7; Length 21;
Best Local Similarity 85.7%; Pred. No. 9.5e+03;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tggcttattcttcag 14
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Db 15 TGGCTTCTGTTTCAG 2

RESULT 15
US-09-379-888B-8
; Sequence 8, Application US/09379888B
; GENERAL INFORMATION:
; APPLICANT: Huan, Bingfang
; APPLICANT: Albagli, David
; APPLICANT: Wood, Michael L.
; APPLICANT: Van Atta, Reuel B.
; APPLICANT: Cheng, Peter C.
; TITLE OF INVENTION: Assays Using Crosslinkable Immobilized Nucleic Acids
; FILE REFERENCE: 14251-0006 CIP
; CURRENT APPLICATION NUMBER: US/09/379,888B
; CURRENT FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: nucleic acid probe
; NAME/KEY: misc_feature
; LOCATION: (1)..(1)
; OTHER INFORMATION: fluorescein attached at 5' end
; NAME/KEY: source
; LOCATION: (1)..(23)
; OTHER INFORMATION: chemically synthesized or biologically prepared nucleic acid
; NAME/KEY: misc_feature
; LOCATION: (22)..(23)
; OTHER INFORMATION: 3-O-(7-coumarinyl)-glycerol between position 22 and 23
US-09-379-888B-8

Query Match 72.0%; Score 10.8; DB 7; Length 23;
Best Local Similarity 85.7%; Pred. No. 9.6e+03;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tggcttattcttcag 14
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Db 5 ttgcttattcttcag 18

Search completed: October 2, 2001, 16:55:07
Job time: 17670 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: October 2, 2001, 21:50:21 ; Search time 17695.9 Seconds
(without alignments)
12.526 Million cell updates/sec

Title: US-09-757-100B-33

Perfect score: 15

Sequence: 1 tqgcttatcttcaqt 15

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scoring table: IDENTITY_NUC
Gapop 10.0 ; Gapext 1.0

Searched: 1415048 seqs, 7388405095 residues

Total number of hits satisfying chosen parameters: 4519004

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

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Maximum Match 100%

Maximum match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	15	100.0	15	1	PCT-US00-18999-33	Sequence 33, Appl	Sequence 33, Appl
2	15	100.0	15	17	US-09-377-310-33	Sequence 33, Appl	Sequence 33, Appl
3	15	100.0	15	29	US-09-757-100B-33	Sequence 33, Appl	Sequence 33, Appl
4	15	100.0	20	1	PCT-US00-18999-13	Sequence 13, Appl	Sequence 13, Appl
5	15	100.0	20	14	US-09-050-392-15	Sequence 15, Appl	Sequence 15, Appl
6	15	100.0	20	17	US-09-377-310-13	Sequence 13, Appl	Sequence 13, Appl
7	15	100.0	20	29	US-09-757-100B-33	Sequence 33, Appl	Sequence 33, Appl
8	13.4	89.3	25	55	US-60-233-166-354400	Sequence 354400, Appl	Sequence 354400, Appl
9	12.4	82.7	18	18	US-09-422-978-3990	Sequence 3990, Appl	Sequence 3990, Appl
10	12.4	82.7	27	6	US-08-292-683-11	Sequence 11, Appl	Sequence 11, Appl
11	12.4	82.7	27	9	US-08-516-859-11	Sequence 11, Appl	Sequence 11, Appl
12	12.4	82.7	27	19	US-09-528-706-11	Sequence 11, Appl	Sequence 11, Appl
13	12.4	82.7	27	22	US-09-586-472-11	Sequence 11, Appl	Sequence 11, Appl
14	12	80.0	18	53	US-60-216-745-7663	Sequence 7663, Appl	Sequence 7663, Appl
15	12	80.0	19	24	US-09-638-509C-18	Sequence 18, Appl	Sequence 18, Appl
16	12	80.0	21	25	US-09-657-472-179	Sequence 179, Appl	Sequence 179, Appl
17	12	80.0	25	55	US-60-234-017-1312510	Sequence 1312510, Appl	Sequence 1312510, Appl
18	12	80.0	25	55	US-60-234-017-469082	Sequence 469082, Appl	Sequence 469082, Appl
19	12	80.0	37	31	US-09-826-509-241	Sequence 241, Appl	Sequence 241, Appl
20	12	80.0	37	31	US-09-826-509-242	Sequence 242, Appl	Sequence 242, Appl
21	11.8	78.7	22	12	US-08-496-155-16	Sequence 16, Appl	Sequence 16, Appl
22	11.8	78.7	22	31	US-09-845-079-16	Sequence 16, Appl	Sequence 16, Appl
23	11.8	78.7	22	31	US-09-852-156-16	Sequence 16, Appl	Sequence 16, Appl
24	11.8	78.7	25	26	US-09-660-220-39947	Sequence 39947, Appl	Sequence 39947, Appl
25	11.8	78.7	25	26	US-09-660-220-52789	Sequence 52789, Appl	Sequence 52789, Appl
26	11.8	78.7	25	26	US-09-660-220-52790	Sequence 52790, Appl	Sequence 52790, Appl
27	11.8	78.7	25	26	US-09-660-220-88553	Sequence 88553, Appl	Sequence 88553, Appl
28	11.8	78.7	25	55	US-60-232-638-79017	Sequence 79017, Appl	Sequence 79017, Appl
29	11.8	78.7	25	55	US-60-232-638-93376	Sequence 93376, Appl	Sequence 93376, Appl
30	11.8	78.7	25	55	US-60-232-638-138151	Sequence 138151, Appl	Sequence 138151, Appl
31	11.8	78.7	25	55	US-60-232-638-138162	Sequence 138162, Appl	Sequence 138162, Appl
32	11.8	78.7	25	55	US-60-233-166-157273	Sequence 157273, Appl	Sequence 157273, Appl
33	11.8	78.7	25	55	US-60-233-166-288539	Sequence 288539, Appl	Sequence 288539, Appl
34	11.8	78.7	25	55	US-60-233-620-26698	Sequence 26698, Appl	Sequence 26698, Appl
35	11.8	78.7	25	55	US-60-234-017-66106	Sequence 66106, Appl	Sequence 66106, Appl
36	11.8	78.7	25	55	US-60-234-017-298566	Sequence 298566, Appl	Sequence 298566, Appl
37	11.8	78.7	25	55	US-60-234-017-411280	Sequence 411280, Appl	Sequence 411280, Appl
38	11.8	78.7	25	55	US-60-234-017-476987	Sequence 476987, Appl	Sequence 476987, Appl
39	11.8	78.7	25	55	US-60-234-017-476988	Sequence 476988, Appl	Sequence 476988, Appl
40	11.8	78.7	25	55	US-60-234-017-490690	Sequence 490690, Appl	Sequence 490690, Appl
41	11.8	78.7	30	4	US-08-037-784-9	Sequence 9, Appl	Sequence 9, Appl
42	11.8	78.7	30	6	US-08-268-880-9	Sequence 9, Appl	Sequence 9, Appl
43	11.8	78.7	30	8	US-08-407-128-10	Sequence 10, Appl	Sequence 10, Appl
44	11.8	78.7	30	8	US-08-409-770-10	Sequence 10, Appl	Sequence 10, Appl</

ALIGNMENTS

RESULT 1
PCT-US00-18999-33
; Sequence 33, Application PC/TUS0018999
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Monia, Brett P.
; APPLICANT: Gaarde, William A.
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
; FILE REFERENCE: ISPH-0476
; CURRENT APPLICATION NUMBER: PCT/US00/18999
; PRIOR FILING DATE: 2000-07-13
; PRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 33
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
PCT-US00-18999-33

Query Match 100.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tggcttatcttcagt 15
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Db 1 tggcttatcttcagt 15

RESULT 2
US-09-377-310-33
; Sequence 33, Application US/09377310A
; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P.
; APPLICANT: Gaarde, William A.
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
; FILE REFERENCE: ISPH-0389
; CURRENT APPLICATION NUMBER: US/09/377,310A
; PRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 33
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
US-09-377-310-33

Query Match 100.0%; Score 15; DB 17; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 tggcttatcttcagt 15

RESULT 3
US-09-757-100B-33
; Sequence 33, Application US/09757100B

; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P.
; APPLICANT: Gaarde, William A.
; APPLICANT: Nero, Pamela S.
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
; FILE REFERENCE: ISPH-0533
; CURRENT APPLICATION NUMBER: US/09/757,100B
; CURRENT FILING DATE: 2001-03-15
; PRIOR FILING DATE: 1999-08-19
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 33
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
US-09-757-100B-33

Query Match 100.0%; Score 15; DB 29; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tggcttatcttcagt 15
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Db 1 tggcttatcttcagt 15

RESULT 4
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; Sequence 13, Application PC/TUS0018999
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Monia, Brett P.
; APPLICANT: Gaarde, William A.
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
; FILE REFERENCE: ISPH-0476
; CURRENT APPLICATION NUMBER: PCT/US00/18999
; CURRENT FILING DATE: 2000-07-13
; PRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
PCT-US00-18999-13

Query Match 100.0%; Score 15; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 3 tggcttatcttcagt 17

RESULT 5
US-09-050-392-15/C
; Sequence 15, Application US/09050392A
; GENERAL INFORMATION:
; APPLICANT: Hasegawa, Osamu

```
; APPLICANT: Aotsuka, Satoshi
; APPLICANT: Hayashi, Takahisa
; APPLICANT: Ihara, Yui
; TITLE OF INVENTION: Cellulose Synthase Gene
; FILE REFERENCE: 20111-0017
; CURRENT APPLICATION NUMBER: US/09/050,392A
; CURRENT FILING DATE: 1998-03-30
; EARLIER APPLICATION NUMBER: JP 9-83133
; EARLIER FILING DATE: 1997-04-01
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-050-392-15

Query Match          100.0%; Score 15; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 16 TGGCTTATCTTCAGT 2

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; Sequence 13, Application US/09377310A
; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P.
; APPLICANT: Gaarde, William A.
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
; FILE REFERENCE: ISPH-0389
; CURRENT APPLICATION NUMBER: US/09/377,310A
; CURRENT FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
US-09-377-310-13

Query Match          100.0%; Score 15; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tggcttatcttcagt 15
Db 3 tggcttatcttcagt 17

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; Sequence 13, Application US/09757100B
; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P.
; APPLICANT: Gaarde, William A.
; APPLICANT: Nero, Pamela S.
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
; FILE REFERENCE: ISPH-0533
; CURRENT APPLICATION NUMBER: US/09/757,100B
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 09/377,310
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; PRIOR FILING DATE: 1999-08-19
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; OTHER INFORMATION: antisense sequence
US-09-757-100b-13

Query Match          100.0%; Score 15; DB 29; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; Sequence 354400, Application US/60233166
; GENERAL INFORMATION:
; APPLICANT: Mittmann
; APPLICANT: Afymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat
; FILE REFERENCE: 3112
; CURRENT APPLICATION NUMBER: US/60/233,166
; CURRENT FILING DATE: 2000-10-24
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; TYPE: DNA
; ORGANISM: Rattus norvegicus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank U65486
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Query Match          89.3%; Score 13.4; DB 55; Length 25;
Best Local Similarity 93.3%; Pred. No. 2.8e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 4 tggcttatcttcagt 18

RESULT 9
US-09-422-978-3990/c
; Sequence 3990, Application US/09422978
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 3990
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; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..18
; OTHER INFORMATION: upstream amplification primer 99-12619 for SEQ 56,
US-09-422-978-3990

Query Match      82.7%; Score 12.4; DB 18; Length 18;
Best Local Similarity 92.9%; Pred. No. 1.le+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 2 ggcttatcttcagt 15
    ||||| |||||
Db 18 GGCATTATTTTCAGT 5

RESULT 10
US-08-292-683-11/c
; Sequence 11, Application US/08292683
; GENERAL INFORMATION:
; APPLICANT: Huang, Shi
; TITLE OF INVENTION: Nucleic Acid Molecules Encoding RIZ
; TITLE OF INVENTION: Protein
; NUMBER OF SEQUENCES: 90
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/292,683
; FILING DATE: 18-AUG-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 1004
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-292-683-11

Query Match      82.7%; Score 12.4; DB 6; Length 27;
Best Local Similarity 92.9%; Pred. No. 1.le+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 tggcttatcttcag 14
    ||||| |||||
Db 27 TGGCTTTTCTTCAG 14

RESULT 11
US-08-516-859-11/c
; Sequence 11, Application US/08516859
; GENERAL INFORMATION:
; APPLICANT: Huang, Shi
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```
; TITLE OF INVENTION: Retinoblastoma Protein - Interacting
; TITLE OF INVENTION: Zinc Finger Proteins
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/516,859
; FILING DATE: 18-AUG-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LA 1776
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-516-859-11

Query Match      82.7%; Score 12.4; DB 9; Length 27;
Best Local Similarity 92.9%; Pred. No. 1.le+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 tggcttatcttcag 14
    ||||| |||||
Db 27 TGGCTTTTCTTCAG 14

RESULT 12
US-09-528-706-11/c
; Sequence 11, Application US/09528706
; GENERAL INFORMATION:
; APPLICANT: Huang, Shi
; TITLE OF INVENTION: Retinoblastoma Protein - Interacting
; TITLE OF INVENTION: Zinc Finger Proteins
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/528,706
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/516,859
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/292,683
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; FILING DATE: 18-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 1776
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-528-706-11

Query Match 82.7%; Score 12.4; DB 19; Length 27;
Best Local Similarity 92.9%; Pred. No. 1.1e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tggcttattctcag 14
||||| |||||||
Db 27 TGGCTTTCTTCAG 14

RESULT 13
US-09-586-472-11/c
; Sequence 11, Application US/09586472
; GENERAL INFORMATION:
; APPLICANT: Huang, Shi
; TITLE OF INVENTION: Retinoblastoma Protein - Interacting
; Zinc Finger Proteins
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/586,472
; FILING DATE: 01-Jun-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/528,706
; FILING DATE: 17-MAR-2000
; APPLICATION NUMBER: US 08/516,859
; FILING DATE: 18-AUG-1995
; APPLICATION NUMBER: US 08/399,411
; FILING DATE: 06-MAR-1995
; APPLICATION NUMBER: US 08/292,683
; FILING DATE: 18-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 4130
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:

US-09-586-472-11

Query Match 82.7%; Score 12.4; DB 22; Length 27;
Best Local Similarity 92.9%; Pred. No. 1.1e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tggcttattctcag 14
||||| |||||||
Db 27 TGGCTTTCTTCAG 14

RESULT 14
US-60-216-745-7663
; Sequence 7663, Application US/60216745
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; APPLICANT: Abderrahim, Hadi
; APPLICANT: Dufauré-Gare, Isabelle
; TITLE OF INVENTION: BIALLELIC MARKER MAPS FOR USE IN CONSTRUCTING A HIGH DENSITY.
; FILE REFERENCE: 84.US1.PRO
; CURRENT APPLICATION NUMBER: US/60/216,745
; CURRENT FILING DATE: 2000-06-30
; NUMBER OF SEQ ID NOS: 13665
; SOFTWARE: Patent.pm
; SEQ ID NO 7663
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..18
; OTHER INFORMATION: upstream amplification primer 99-46755 for SEQ 3132,
US-60-216-745-7663

Query Match 80.0%; Score 12; DB 53; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.7e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 cttattctcagt 15
||||| |||||||
Db 3 cttattctcagt 14

RESULT 15
US-09-638-509C-18/c
; Sequence 18, Application US/09638509C
; GENERAL INFORMATION:
; APPLICANT: Tang, Jianming
; APPLICANT: Kaslow, Richard A.
; TITLE OF INVENTION: Methods of Surveying For CC (Beta) Chemokine
; TITLE OF INVENTION: Receptor Variants and Their Association With HIV-1
; TITLE OF INVENTION: Transmission and/or Disease Progression
; FILE REFERENCE: D6217
; CURRENT APPLICATION NUMBER: US/09/638,509C
; CURRENT FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/148,530
; PRIOR FILING DATE: 1999-08-12
; NUMBER OF SEQ ID NOS: 35
; SEQ ID NO 18
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: primer_bind
; OTHER INFORMATION: CCR5-PM6G, primer used for typing major
; OTHER INFORMATION: polymorphism in CCR2b, CCR5 and the CCR5 downstream
; OTHER INFORMATION: promoter region
US-09-638-509C-18

Query Match 80.0%; Score 12; DB 24; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.7e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ggcttatcttca 13
|||
Db 15 GGCTTATCTTCA 4

Search completed: October 2, 2001, 21:50:22
Job time: 24535 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: October 2, 2001, 16:55:07 ; Search time 2173.58 Seconds
(without alignments)
14.467 Million cell updates/sec

Title: US-09-757-100B-31

Perfect score: 15

Sequence: 1 taccagggtgagtct 15

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1895189 seqs, 1048201267 residues

Total number of hits satisfying chosen parameters: 299022

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending_Patents_NA_New:*

- 1: /cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq:*
- 2: /cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq:*
- 3: /cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq:*
- 4: /cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq:*
- 5: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:*
- 6: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:*
- 7: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:*
- 8: /cgn2_6/ptodata/2/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	12.4	82.7	33	7	US-09-672-217-122
2	12.4	82.7	33	7	US-09-672-217-223
3	11.4	76.0	25	6	US-09-857-581-65
4	11.4	76.0	31	6	US-09-801-274-1705
5	10.8	72.0	27	7	US-09-794-384A-10
6	10.4	69.3	15	5	US-09-406-643-4
7	10.4	69.3	15	5	US-09-406-643-293
8	10.4	69.3	15	5	US-09-406-643-294
9	10.4	69.3	17	6	US-09-866-108-7712
10	10.4	69.3	17	6	US-09-866-108-7713
11	10.4	69.3	17	6	US-09-866-108-7714
12	10.4	69.3	17	6	US-09-866-108-7715
13	10.4	69.3	17	6	US-09-866-108-7716
14	10.4	69.3	17	6	US-09-866-108-7717
15	10.4	69.3	19	5	US-09-927-796-165
16	10.4	69.3	19	5	US-09-927-796-168
17	10.4	69.3	20	1	PCT-US01-25860-20
18	10.4	69.3	25	6	US-09-866-108-12604
19	10.4	69.3	25	6	US-09-866-108-12605
20	10.4	69.3	25	6	US-09-866-108-12606
21	10.4	69.3	25	6	US-09-866-108-12607
22	10.4	69.3	25	6	US-09-866-108-12608
23	10.4	69.3	25	6	US-09-866-108-12609
24	10.4	69.3	25	6	US-09-866-108-12610
25	10.4	69.3	25	6	US-09-866-108-12611

26	10.4	69.3	25	6	US-09-866-108-12612	Sequence 12612, A
27	10.4	69.3	25	6	US-09-866-108-12613	Sequence 12613, A
28	10.4	69.3	25	6	US-09-866-108-12614	Sequence 12614, A
29	10.4	69.3	25	6	US-09-866-108-12615	Sequence 12615, A
30	10.4	69.3	25	6	US-09-866-108-12616	Sequence 12616, A
31	10.4	69.3	25	6	US-09-866-108-12617	Sequence 12617, A
32	10.4	69.3	26	7	US-09-735-271-1624	Sequence 1624, Ap
33	10.4	69.3	31	6	US-09-817-879-5614	Sequence 5614, Ap
34	10.4	69.3	48	8	US-60-253-457-42408	Sequence 42408, A
35	10.4	69.3	49	8	US-60-278-258-16237	Sequence 16237, A
36	10.4	69.3	50	8	US-60-252-833-30106	Sequence 30106, A
37	10.2	68.0	20	6	US-09-801-968-13	Sequence 13, Appl
38	10.2	68.0	20	7	US-09-844-353A-10	Sequence 10, Appl
39	10.2	68.0	22	7	US-09-648-103B-51	Sequence 51, Appl
40	10.2	68.0	25	7	US-09-648-103B-49	Sequence 49, Appl
41	10.2	68.0	47	8	US-60-278-232-10744	Sequence 10744, A
42	10	66.7	12	5	US-09-481-375-29	Sequence 29, Appl
43	10	66.7	12	5	US-09-479-122-29	Sequence 29, Appl
44	10	66.7	17	6	US-09-866-108-1321	Sequence 1321, Ap
45	10	66.7	17	6	US-09-866-108-1322	Sequence 1322, Ap

ALIGNMENTS

RESULT 1
US-09-672-217-122
; Sequence 122, Application US/09672217
; GENERAL INFORMATION:
; APPLICANT: FELL, JACK
; APPLICANT: DIAZ, MARA
; APPLICANT: MCABE, MEADE
; TITLE OF INVENTION: METHOD OF IDENTIFYING PATHOGENIC CRYPTOCOCCI
; FILE REFERENCE: 086222/0143
; CURRENT APPLICATION NUMBER: US/09/672,217
; CURRENT FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/156,598
; PRIOR FILING DATE: 1999-09-29
; NUMBER OF SEQ ID NOS: 301
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 122
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer/Probe
US-09-672-217-122

Query Match 82.7%; Score 12.4; DB 7; Length 33;
Best Local Similarity 92.9%; Pred. No. 1.le+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 acccagggtgagtct 15
Db 17 acccagggtgagtat 30
|||||

RESULT 2
US-09-672-217-223
; Sequence 223, Application US/09672217
; GENERAL INFORMATION:
; APPLICANT: FELL, JACK
; APPLICANT: DIAZ, MARA
; APPLICANT: MCABE, MEADE
; TITLE OF INVENTION: METHOD OF IDENTIFYING PATHOGENIC CRYPTOCOCCI
; FILE REFERENCE: 086222/0143
; CURRENT APPLICATION NUMBER: US/09/672,217
; CURRENT FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/156,598
; PRIOR FILING DATE: 1999-09-29
; NUMBER OF SEQ ID NOS: 301
; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 223
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer/Probe
US-09-672-217-223

Query Match 82.7%; Score 12.4; DB 7; Length 33;
Best Local Similarity 92.9%; Pred. No. 1.1e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 acccaggtgagtct 15
|||||

Db 17 acccaggtgagtct 30
|||||

RESULT 3
US-09-857-581-65/c
; Sequence 65, Application US/09857581
; GENERAL INFORMATION:
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
; FILE REFERENCE: BB1339 PCT
; CURRENT APPLICATION NUMBER: US/09/857,581
; CURRENT FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: 60/117,769
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: 60/144,783
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/156,094
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 65
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: PCR PRIMER
US-09-857-581-65

Query Match 76.0%; Score 11.4; DB 6; Length 25;
Best Local Similarity 92.3%; Pred. No. 4.2e+03;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 cccaggtgagtct 15
|||||

Db 17 CCCAGGTGAGTTT 5
|||||

RESULT 4
US-09-801-274-1705/c
; Sequence 1705, Application US/09801274
; GENERAL INFORMATION:
; APPLICANT: Cargill, Michele
; APPLICANT: Ireland, James S.
; APPLICANT: Lander, Eric S.
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: 2825.2009-001
; CURRENT APPLICATION NUMBER: US/09/801,274
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: US 60/187,510
; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: US 60/206,129
; PRIOR FILING DATE: 2000-05-22
; NUMBER OF SEQ ID NOS: 1802
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1705
; LENGTH: 31
; TYPE: DNA

; ORGANISM: Homo sapiens
US-09-801-274-1705

Query Match 76.0%; Score 11.4; DB 6; Length 31;
Best Local Similarity 92.3%; Pred. No. 4.3e+03;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 cccaggtgagtct 15
|||||

Db 14 CCCAGCTGAGTCT 2
|||||

RESULT 5
US-09-794-384A-10
; Sequence 10, Application US/09794384A
; GENERAL INFORMATION:
; APPLICANT: Dellaporta, Stephen L.
; APPLICANT: Moreno, Maria A.
; APPLICANT: Yale University
; TITLE OF INVENTION: Methods and Compositions to Reduce or Eliminate
; FILE REFERENCE: 44574-5078-US
; CURRENT APPLICATION NUMBER: US/09/794,384A
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 60/185,524
; PRIOR FILING DATE: 2000-02-28
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 27
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: 5' PCR primer
US-09-794-384A-10

Query Match 72.0%; Score 10.8; DB 7; Length 27;
Best Local Similarity 85.7%; Pred. No. 9.7e+03;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 acccaggtgagtct 15
|||||

Db 1 acccaggtgagttt 14
|||||

RESULT 6
US-09-406-643-4/c
; Sequence 4, Application US/09406643
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Ludwig, Janos
; APPLICANT: Sproat, Brian
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: Compositions Having RNA Cleaving Activity
; FILE REFERENCE: MBHB00-874-A (237/197)
; CURRENT APPLICATION NUMBER: US/09/406,643
; CURRENT FILING DATE: 1999-09-27
; PRIOR APPLICATION NUMBER: US 08/879,078
; PRIOR FILING DATE: 1997-06-19
; PRIOR APPLICATION NUMBER: US 08/878,640
; PRIOR FILING DATE: 1997-06-19
; NUMBER OF SEQ ID NOS: 2606
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-406-643-4

Query Match 69.3%; Score 10.4; DB 5; Length 15;

Best Local Similarity 91.7%; Pred. No. 1.6e+04;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 ccaggtgagtc 15
||||||| |||||

Db 15 CCAGGTGGGTCT 4

RESULT 7
US-09-406-643-293/C
; Sequence 293, Application US/09406643
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Ludwig, Janos
; APPLICANT: Sproat, Brian
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: Compositions Having RNA Cleaving Activity
; FILE REFERENCE: MBH00-874-A (237/197)
; CURRENT APPLICATION NUMBER: US/09/406,643
; CURRENT FILING DATE: 1999-09-27
; PRIOR FILING DATE: 1997-06-19
; PRIOR APPLICATION NUMBER: US 08/879,078
; PRIOR FILING DATE: 1997-06-19
; PRIOR APPLICATION NUMBER: US 08/878,640
; PRIOR FILING DATE: 1997-06-19
; NUMBER OF SEQ ID NOS: 2606
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 293
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-406-643-293

Query Match 69.3%; Score 10.4; DB 5; Length 15;
Best Local Similarity 91.7%; Pred. No. 1.6e+04;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 ccaggtgagtc 15
||||||| |||||

Db 14 CCAGGTGGGTCT 3

RESULT 8
US-09-406-643-294/C
; Sequence 294, Application US/09406643
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Ludwig, Janos
; APPLICANT: Sproat, Brian
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: Compositions Having RNA Cleaving Activity
; FILE REFERENCE: MBH00-874-A (237/197)
; CURRENT APPLICATION NUMBER: US/09/406,643
; CURRENT FILING DATE: 1999-09-27
; PRIOR FILING DATE: 1997-06-19
; PRIOR APPLICATION NUMBER: US 08/879,078
; PRIOR FILING DATE: 1997-06-19
; PRIOR APPLICATION NUMBER: US 08/878,640
; NUMBER OF SEQ ID NOS: 2606
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 294
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-406-643-294

Query Match 69.3%; Score 10.4; DB 5; Length 15;
Best Local Similarity 91.7%; Pred. No. 1.6e+04;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 ccaggtgagtc 15
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Db 13 CCAGGTGGGTCT 2

RESULT 9
US-09-866-108-7712
; Sequence 7712, Application US/098666108
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
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; PRIOR FILING DATE: 2001-01-30
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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 7712
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-7712

Query Match 69.3%; Score 10.4; DB 6; Length 17;
Best Local Similarity 91.7%; Pred. No. 1.6e+04;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 ccaggtgagtc 14
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Db 6 cctaggtgagtc 17

RESULT 10
US-09-866-108-7713
; Sequence 7713, Application US/098666108
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.

Query Match 69.3%; Score 10.4; DB 6;
Best Local Similarity 91.7%; Pred. No. 1.6e+04;
Matches 11; Conservative 0; Mismatches 1; Indels

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RESULT 12
US-09-866-108-7715
; Sequence 7715, Application US/09866108
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSION
; FILE REFERENCE: ABOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIORITY APPLICATION NUMBER: US 60/207,456
; PRIORITY FILING DATE: 2000-05-26
; PRIORITY APPLICATION NUMBER: GB 24263.6
; PRIORITY FILING DATE: 2000-10-04
; PRIORITY APPLICATION NUMBER: US 60/236,359
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; PRIORITY FILING DATE: 2001-01-30
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; PRIORITY FILING DATE: 2001-01-30
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, , NUMBER OF SEQ ID NOS: 15752
, , SOFTWARE: Aecomica Sequence Listing Engine
, , SEQ ID NO 7715
, , LENGTH: 17
, , TYPE: DNA
, , ORGANISM: Homo sapiens
US-09-866-108-7715

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Query Match	69.3%	Score 10.4;	DB 6;	Length 17;
Best Local Similarity	91.7%	Pred. No. 1.6e+04;		
Matches 11; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;

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; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 7716
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-7716

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Query Match	69.3%	Score 10.4;	DB 6;	Length 17;
Best Local Similarity	91.7%	Pred. No. 1.6e+04;		
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-7717

Query Match      69.3%   Score 10.4;   DB 6;   Length 17;
Best Local Similarity 91.7%;   Pred. No. 1.6e+04;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 cccaggtgagtc 14
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Db 1 cctaggtgagtc 12

RESULT 15
US-09-927-796-165
; Sequence 165, Application US/09927796
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Marsters, Scot A.
; APPLICANT: Pan, James
; APPLICANT: Pitti, Robert M.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Smith, Victoria
; APPLICANT: Stone, Donna M.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT OF TUMOR
; FILE REFERENCE: P2531R1C1
; CURRENT APPLICATION NUMBER: US/09/927,796
; CURRENT FILING DATE: 2001-08-09
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;; PRIOR FILING DATE: 2001-07-09
;; NUMBER OF SEQ ID NOS: 258
;; SEQ ID NO 165
;; LENGTH: 19

Query Match 69.3%; Score 10.4; DB 5; Length 19;
Best Local Similarity 91.7%; Pred. No. 1.6e+04;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Caps 0;

Qy 3 cccaggtgagtc 14
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Db 5 ccaagtgagtc 16

Search completed: October 2, 2001, 16:55:07
Job time: 17670 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 2, 2001, 21:50:20 ; Search time 17695.9 Seconds
(without alignments)
12.526 Million cell updates/sec

Title: US-09-757-100B-31

Perfect score: 15

Sequence: 1 taccacagtgagtct 15

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 14155048 seqs, 7388405095 residues

Total number of hits satisfying chosen parameters: 4519004

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	15	100.0	20	1	PCT-US00-18999-11
5	15	100.0	20	17	US-09-377-310-11
6	15	100.0	20	29	US-09-757-100B-11
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8	12.4	82.7	21	3	US-07-918-259-7
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26	11.8	78.7	25	55	US-60-233-166-320910
27	11.8	78.7	25	55	US-60-233-166-334434
28	11.8	78.7	25	55	US-60-233-166-379370
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33	11.8	78.7	25	55	US-60-234-017-22548
34	11.8	78.7	25	55	US-60-234-017-142091
35	11.8	78.7	25	55	US-60-234-017-147526
36	11.8	78.7	25	55	US-60-234-017-270612
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38	11.8	78.7	25	55	US-60-234-017-296787
39	11.8	78.7	25	55	US-60-234-017-365211
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41	11.8	78.7	25	55	US-60-234-017-536143
42	11.8	78.7	25	55	US-60-234-017-536147
43	11.8	78.7	34	16	US-09-214-151-3
44	11.8	78.7	48	18	US-09-404-520-33931
45	11.4	76.0	18	3	US-07-674-366-33

ALIGNMENTS

RESULT 1
PCT-US00-18999-31
; Sequence 31, Application PC/TUS0018999
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Monia, Brett P.
; APPLICANT: Gaarde, William A.
; APPLICANT: Nero, Pamela S.
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
; FILE REFERENCE: ISPH-0476
; CURRENT APPLICATION NUMBER: PCT/US00/18999
; CURRENT FILING DATE: 2000-07-13
; PRIOR APPLICATION NUMBER: 09/377,310
; PRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 31
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
PCT-US00-18999-31

Query Match 100.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 taccagggtgagctct 15
Db 1 taccagggtgagctct 15

RESULT 2
US-09-377-310-31
; Sequence 31, Application US/09377310A
; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P.
; APPLICANT: Gaarde, William A.
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
; FILE REFERENCE: ISPH-0389
; CURRENT APPLICATION NUMBER: US/09/377,310A
; CURRENT FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 31
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
US-09-377-310-31

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Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 taccagggtgagctct 15
Db 1 taccagggtgagctct 15

RESULT 3
US-09-757-100B-31
; Sequence 31, Application US/09757100B

; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P.
; APPLICANT: Gaarde, William A.
; APPLICANT: Nero, Pamela S.
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
; FILE REFERENCE: ISPH-0533
; CURRENT APPLICATION NUMBER: US/09/757,100B
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 09/377,310
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/US00/18999
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 31
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
US-09-757-100B-31

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Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 taccagggtgagctct 15
Db 1 taccagggtgagctct 15

RESULT 4
PCT-US00-18999-11
; Sequence 11, Application PC/TUS0018999
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Monia, Brett P.
; APPLICANT: Gaarde, William A.
; APPLICANT: Nero, Pamela S.
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
; FILE REFERENCE: ISPH-0476
; CURRENT APPLICATION NUMBER: PCT/US00/18999
; CURRENT FILING DATE: 2000-07-13
; PRIOR APPLICATION NUMBER: 09/377,310
; PRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
PCT-US00-18999-11

Query Match 100.0%; Score 15; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 taccagggtgagctct 15
Db 3 taccagggtgagctct 17

RESULT 5
US-09-377-310-11
; Sequence 11, Application US/09377310A
; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P.


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; CURRENT APPLICATION NUMBER: US/60/233,166
; CURRENT FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 420907
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 293033
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank AI639536
US-60-233-166-293033

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Best Local Similarity 92.9%; Pred. No. 8.5e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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; Sequence 93096, Application US/60234017
; GENERAL INFORMATION:
; APPLICANT: Mittmann, M
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of Mus
; FILE REFERENCE: 3115
; CURRENT APPLICATION NUMBER: US/60/234,017
; CURRENT FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 605887
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 93096
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank AI854595
US-60-234-017-93096

Query Match      82.7%; Score 12.4; DB 55; Length 25;
Best Local Similarity 92.9%; Pred. No. 8.5e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 taccagggtgagtc 14
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RESULT 13
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; Sequence 150700, Application US/60234017
; GENERAL INFORMATION:
; APPLICANT: Mittmann, M
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of Mus
; FILE REFERENCE: 3115
; CURRENT APPLICATION NUMBER: US/60/234,017
; CURRENT FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 605887
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 150700
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank AI849180
US-60-234-017-150700

; CURRENT APPLICATION NUMBER: US/60/233,166
; CURRENT FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 420907
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 72838
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank AA819408
US-60-233-166-72838

Query Match      82.7%; Score 12.4; DB 55; Length 25;
Best Local Similarity 92.9%; Pred. No. 8.5e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 acccagggtgagtc 15
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Db 10 accaagggtgagtc 23

RESULT 10
US-60-233-166-188071
; Sequence 188071, Application US/60233166
; GENERAL INFORMATION:
; APPLICANT: Mittmann
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat
; FILE REFERENCE: 3112
; CURRENT APPLICATION NUMBER: US/60/233,166
; CURRENT FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 420907
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 188071
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank AA963963
US-60-233-166-188071

Query Match      82.7%; Score 12.4; DB 55; Length 25;
Best Local Similarity 92.9%; Pred. No. 8.5e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 acccagggtgagtc 15
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Db 4 acccaggtaagtc 17

RESULT 11
US-60-233-166-293033/c
; Sequence 293033, Application US/60233166
; GENERAL INFORMATION:
; APPLICANT: Mittmann
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat
; FILE REFERENCE: 3112
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Query Match 82.7%; Score 12.4; DB 55; Length 25;
Best Local Similarity 92.9%; Pred. No. 8.5e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 acccaggtgagtct 15
||| |||||
Db 10 accaagtgagtct 23

RESULT 14

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; Sequence 150701, Application US/60234017
; GENERAL INFORMATION:
; APPLICANT: Mittmann, M
; TITLE OF INVENTION: Methods of Genetic Analysis of Mus
; FILE REFERENCE: 3115
; CURRENT APPLICATION NUMBER: US/60/234,017
; CURRENT FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 605887
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 150701
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank AF849180
US-60-234-017-150701

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Best Local Similarity 92.9%; Pred. No. 8.5e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 7 accaagtgagtct 20

RESULT 15

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; Sequence 449268, Application US/60234017
; GENERAL INFORMATION:
; APPLICANT: Mittmann, M
; TITLE OF INVENTION: Methods of Genetic Analysis of Mus
; FILE REFERENCE: 3115
; CURRENT APPLICATION NUMBER: US/60/234,017
; CURRENT FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 605887
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 449268
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank AW123353
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Query Match 82.7%; Score 12.4; DB 55; Length 25;
Best Local Similarity 92.9%; Pred. No. 8.5e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 acccaggtgagtct 15
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Db 2 accaagtgagtct 15

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

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Title: US-09-757-100B-30

Perfect score: 15

Sequence: 1 taagcagctgccatt 15

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 14155048 seqs, 7388405095 residues

Total number of hits satisfying chosen parameters: 4519004

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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3		15	100.0	15	29	US-09-757-100B-30				Sequence 30, Appl	
4		15	100.0	20	1	PCT-US00-18999-10				Sequence 10, Appl	
5		15	100.0	20	17	US-09-377-310-10				Sequence 10, Appl	
6		15	100.0	20	29	US-09-757-100B-10				Sequence 10, Appl	
C 7		13.4	89.3	18	7	US-08-378-761-45				Sequence 45, Appl	
C 8		12.4	82.7	24	1	PCT-US01-06413-8				Sequence 8, Appl	
C 9		12.4	82.7	25	55	US-60-234-049-76441				Sequence 76441, A	
C 10		12.4	82.7	27	16	US-09-218-207-173				Sequence 173, Appl	
C 11		12.4	82.7	27	17	US-09-338-907-173				Sequence 173, Appl	
C 12		12.4	82.7	49	19	US-09-507-691-6				Sequence 6, Appl	
C 13		12	80.0	15	1	PCT-US01-05126-13				Sequence 13, Appl	
C 14		12	80.0	25	55	US-60-233-620-95891				Sequence 95891, A	
C 15		12	80.0	25	55	US-60-233-620-111530				Sequence 111530, A	
C 16		12	80.0	32	11	US-08-700-519F-5				Sequence 5, Appl	
C 17		12	80.0	32	11	US-08-700-519I-5				Sequence 5, Appl	
C 18		12	80.0	32	11	US-08-700-519J-5				Sequence 5, Appl	
C 19		12	80.0	39	16	US-09-211-424-18				Sequence 18, Appl	
C 20		12	80.0	47	53	US-60-216-745-4119				Sequence 4119, Appl	
C 21		11.8	78.7	21	57	US-60-259-128-3252				Sequence 3252, Appl	
C 22		11.8	78.7	25	55	US-60-232-638-20692				Sequence 20692, A	
C 23		11.8	78.7	25	55	US-60-232-638-75827				Sequence 75827, A	
C 24		11.8	78.7	25	55	US-60-233-620-13224				Sequence 13224, A	
C 25		11.8	78.7	25	55	US-60-234-017-432078				Sequence 432078, A	
C 26		11.8	78.7	25	55	US-60-234-017-432084				Sequence 432084, A	
C 27		11.8	78.7	25	55	US-60-234-017-432087				Sequence 432087, A	
C 28		11.8	78.7	25	55	US-60-234-017-432091				Sequence 432091, A	
C 29		11.8	78.7	25	55	US-60-234-017-502150				Sequence 502150, A	
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C 34		11.8	78.7	50	8	US-08-475-228-487				Sequence 487, App	
C 35		11.8	78.7	50	8	US-08-482-080-486				Sequence 486, App	
C 36		11.8	78.7	50	8	US-08-482-080-487				Sequence 487, App	
C 37		11.8	78.7	50	16	US-09-270-849B-135913				Sequence 135913, A	
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C 39		11.8	78.7	50	17	US-09-354-947-487				Sequence 487, App	
C 40		11.6	77.3	29	17	US-09-304-232-241				Sequence 241, App	
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C 43		11.4	76.0	20	9	US-08-531-241A-1215				Sequence 1215, Ap	
C 44		11.4	76.0	20	12	US-08-832-658-4				Sequence 4, Appli	
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ALIGNMENTS

RESULT 1
PCT-US00-18999-30
; Sequence 30, Application PC/TUS0018999
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Monia, Brett P.
; APPLICANT: Gaarde, William A.
; APPLICANT: Nero, Pamela S.
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
; FILE REFERENCE: ISPH-0476
; CURRENT FILING DATE: 2000-07-13
; PRIOR APPLICATION NUMBER: PCT/US00/18999
; PRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
PCT-US00-18999-30

Query Match 100.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 ||||| ||||| |||||

RESULT 2
US-09-377-310-30
; Sequence 30, Application US/09377310A
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Monia, Brett P.
; APPLICANT: Gaarde, William A.
; APPLICANT: Nero, Pamela S.
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
; FILE REFERENCE: ISPH-0389
; CURRENT FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: US/09/377,310A
; PRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
US-09-377-310-30

Query Match 100.0%; Score 15; DB 17; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 taagcagctgccatt 15
Db 1 ||||| ||||| |||||

RESULT 3
US-09-757-100B-30
; Sequence 30, Application US/09757100B

; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P.
; APPLICANT: Gaarde, William A.
; APPLICANT: Nero, Pamela S.
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
; FILE REFERENCE: ISPH-0533
; CURRENT APPLICATION NUMBER: US/09/757,100B
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 09/377,310
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/US00/18999
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
US-09-757-100B-30

Query Match 100.0%; Score 15; DB 29; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 taagcagctgccatt 15
Db 1 ||||| ||||| |||||

RESULT 4
PCT-US00-18999-10
; Sequence 10, Application PC/TUS0018999
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Monia, Brett P.
; APPLICANT: Gaarde, William A.
; APPLICANT: Nero, Pamela S.
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
; FILE REFERENCE: ISPH-0476
; CURRENT APPLICATION NUMBER: PCT/US00/18999
; CURRENT FILING DATE: 2000-07-13
; PRIOR APPLICATION NUMBER: 09/377,310
; PRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
PCT-US00-18999-10

Query Match 100.0%; Score 15; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 taagcagctgccatt 15
Db 3 taagcagctgccatt 17

RESULT 5
US-09-377-310-10
; Sequence 10, Application US/09377310A
; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P.

APPLICANT: Gaarde, William A.
TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
FILE REFERENCE: ISPH-0389
CURRENT APPLICATION NUMBER: US/09/377,310A
CURRENT FILING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 10
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: antisense sequence
US-09-377-310-10

Query Match 100.0%; Score 15; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 taagcagctgccatt 15
|||||

Db 3 taagcagctgccatt 17
|||||

RESULT 6

US-09-757-100b-10
Sequence 10, Application US/09757100B
GENERAL INFORMATION:
APPLICANT: Monia, Brett P.
APPLICANT: Gaarde, William A.
APPLICANT: Nero, Pamela S.
TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
FILE REFERENCE: ISPH-0533
CURRENT APPLICATION NUMBER: US/09/757,100B
CURRENT FILING DATE: 2001-03-15
PRIOR APPLICATION NUMBER: 09/377,310
PRIOR FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/US00/18999
PRIOR FILING DATE: 2000-07-13
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 10
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: antisense sequence
US-09-757-100b-10

Query Match 100.0%; Score 15; DB 29; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 taagcagctgccatt 15
|||||

Db 3 taagcagctgccatt 17
|||||

RESULT 7

US-08-378-761-45/c
Sequence 45, Application US/08378761
GENERAL INFORMATION:
APPLICANT: WALSH, TERENCE A
APPLICANT: HEY, TIMOTHY D
APPLICANT: MORGAN, ALICE ER
TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
TITLE OF INVENTION: USING
NUMBER OF SEQUENCES: 59

CORRESPONDENCE ADDRESS:
ADDRESSEE: THOMAS D. ZINDRICK
STREET: 9002 PURDUE ROAD
CITY: INDIANAPOLIS
STATE: IN
COUNTRY: US
ZIP: 46268-1189
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/378,761
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/987927
FILING DATE: 09-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: ZINDRICK, THOMAS D
REGISTRATION NUMBER: 32185
REFERENCE/DOCKET NUMBER: 38272A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (517) 636-1869
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-378-761-45

Query Match 89.3%; Score 13.4; DB 7; Length 18;
Best Local Similarity 93.3%; Pred. No. 3.7e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 taagcagctgccatt 15
|||||

Db 17 TAAGCAGCTGCAATT 3
|||||

RESULT 8

PCT-US01-06413-8/c
Sequence 8, Application PC/TUS0106413
GENERAL INFORMATION:
APPLICANT: The General Hospital Corporation
TITLE OF INVENTION: BETA NETRIN AND USES THEREOF
FILE REFERENCE: 10287-057W01
CURRENT APPLICATION NUMBER: PCT/US01/06413
CURRENT FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: US 60/185,811
PRIOR FILING DATE: 2000-02-29
PRIOR APPLICATION NUMBER: US 60/229,893
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8
LENGTH: 24
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: primer for PCR
PCT-US01-06413-8

Query Match 82.7%; Score 12.4; DB 1; Length 24;
Best Local Similarity 92.9%; Pred. No. 1.4e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 aagcagctgccatt 15
|||||

Db 21 AAGCAGCTGCCCTT 8

RESULT 9

US-60-234-049-76441/c
; Sequence 76441, Application US/60234049
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of
; TITLE OF INVENTION: Escherichia coli
; FILE REFERENCE: 3117
; CURRENT APPLICATION NUMBER: US/60/234,049
; EARLIER FILING DATE: 2000-09-19
; NUMBER OF SEQ ID NOS: 141629
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 76441
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Escherichia coli
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank U00096
US-60-234-049-76441

Query Match 82.7%; Score 12.4; DB 55; Length 25;
Best Local Similarity 92.9%; Pred. No. 1.4e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 aagcagctgccatt 15

Db 18 AAGCTGCTGCCATT 5
||||| |||||||

RESULT 10

US-09-218-207-173/c
; Sequence 173, Application US/09218207
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Ilya, Chumakov
; APPLICANT: Bougueleret, Lydie
; TITLE OF INVENTION: Prostate cancer gene
; FILE REFERENCE: GENSET.018CPI
; CURRENT APPLICATION NUMBER: US/09/218,207
; EARLIER FILING DATE: 1998-12-22
; EARLIER APPLICATION NUMBER: 08/996,306
; EARLIER FILING DATE: 1997-12-22
; EARLIER APPLICATION NUMBER: 60/099,658
; EARLIER FILING DATE: 1998-09-09
; NUMBER OF SEQ ID NOS: 578
; SOFTWARE: Patent.pm
; SEQ ID NO 173
; LENGTH: 27
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 1..27
; OTHER INFORMATION: amplification oligonucleotide PGIa5b8
US-09-218-207-173

Query Match 82.7%; Score 12.4; DB 16; Length 27;
Best Local Similarity 92.9%; Pred. No. 1.4e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 taagcagctgccat 14

Db 24 TAAGCATCTGCCAT 11
||||| |||||||

RESULT 11

US-09-338-907-173/c
; Sequence 173, Application US/09338907
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Ilya, Chumakov
; APPLICANT: Bougueleret, Lydie
; TITLE OF INVENTION: PROSTATE CANCER GENE
; FILE REFERENCE: GENSET.18CPICP
; CURRENT APPLICATION NUMBER: US/09/338,907
; CURRENT FILING DATE: 1999-06-23
; EARLIER APPLICATION NUMBER: 08/996,306
; EARLIER FILING DATE: 1997-12-22
; EARLIER APPLICATION NUMBER: 60/099,658
; EARLIER FILING DATE: 1998-09-09
; EARLIER APPLICATION NUMBER: 09/218,207
; EARLIER FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 578
; SOFTWARE: Patent.pm
; SEQ ID NO 173
; LENGTH: 27
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 1..27
; OTHER INFORMATION: amplification oligonucleotide PGIa5b8
US-09-338-907-173

Query Match 82.7%; Score 12.4; DB 17; Length 27;
Best Local Similarity 92.9%; Pred. No. 1.4e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 taagcagctgccat 14

Db 24 TAAGCATCTGCCAT 11
||||| |||||||

RESULT 12

US-09-507-691-6/c
; Sequence 6, Application US/09507691
; GENERAL INFORMATION:
; APPLICANT: ISHIKAWA, Tetsuya
; APPLICANT: KITAJIMA, Takashi
; TITLE OF INVENTION: COLLAGEN-BINDING PHYSIOLOGICALLY ACTIVE POLYPEPTIDE
; FILE REFERENCE: 029650-087
; CURRENT APPLICATION NUMBER: US/09/507,691
; CURRENT FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: JP 11-041913
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: JP 11-311364
; PRIOR FILING DATE: 1999-11-01
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 49
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:PCR sense
; OTHER INFORMATION: primer for human fibronectin collagen-binding
; OTHER INFORMATION: domain
US-09-507-691-6

Query Match 82.7%; Score 12.4; DB 19; Length 49;
Best Local Similarity 92.9%; Pred. No. 1.6e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 taagcagctgccat 14

Db 31 TAAGCAGCTGCCAT 18
||| |||||||||

RESULT 13
PCT-US01-05126-13/C
; Sequence 13, Application PC/TUS0105126
; GENERAL INFORMATION:
; APPLICANT: Denton, Richard R
; APPLICANT: Nandabalan, Krishnan
; APPLICANT: Chew, Anne
; APPLICANT: Choi, Julie
; APPLICANT: Stephens, J. Claiborne
; APPLICANT: Genesense Pharmaceuticals, Inc.
; TITLE OF INVENTION: Haplotypes of the PON1 Gene
; FILE REFERENCE: PONI1PCT
; CURRENT APPLICATION NUMBER: PCT/US01/05126
; CURRENT FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: 60/182,930
; PRIOR FILING DATE: 2000-02-16
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US01-05126-13

Query Match 80.0%; Score 12; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 2.2e+04;
Matches 12; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 aagcagctgccatt 15
|:|||||||
Db 15 AWGAGCTGGCATT 2

RESULT 14
US-60-233-620-95891
; Sequence 95891, Application US/60233620
; GENERAL INFORMATION:
; APPLICANT: Mittmann
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of
; Arabidopsis thaliana
; FILE REFERENCE: 3116
; CURRENT APPLICATION NUMBER: US/60/233,620
; CURRENT FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 131820
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 95891
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank AC007591
US-60-233-620-95891

Query Match 80.0%; Score 12; DB 55; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.4e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 taagcagctgcc 12
|:|||||||
Db 13 taagcagctgcc 24

RESULT 15
US-60-233-620-111530
; Sequence 111530, Application US/60233620
; GENERAL INFORMATION:
; APPLICANT: Mittmann
; APPLICANT: Affymetrix, Inc.

Query Match 80.0%; Score 12; DB 55; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.4e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 taagcagctgcc 12
|:|||||||
Db 10 taagcagctgcc 21

Search completed: October 2, 2001, 21:50:20.
Job time: 24533 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: October 2, 2001, 16:55:06 ; Search time 2173.58 Seconds
(without alignments)
14.467 Million cell updates/sec

Title: US-09-757-100B-30
Perfect score: 15
Sequence: 1 taagcagctgccatt 15

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1895189 seqs, 1048201267 residues

Total number of hits satisfying chosen parameters: 299022

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_NA_New:*
1: /cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq:*
2: /cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq:*
3: /cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq:*
4: /cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq:*
5: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:*
6: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq1:*
7: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq2:*
8: /cgn2_6/ptodata/2/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
C 1	12	80.0	17	6	US-09-866-108-7017
C 2	12	80.0	17	6	US-09-866-108-7018
C 3	12	80.0	17	6	US-09-866-108-7019
C 4	12	80.0	17	6	US-09-866-108-7020
C 5	12	80.0	17	6	US-09-866-108-7021
C 6	12	80.0	17	6	US-09-866-108-7022
C 7	12	80.0	25	6	US-09-866-108-11909
C 8	12	80.0	25	6	US-09-866-108-11910
C 9	12	80.0	25	6	US-09-866-108-11911
C 10	12	80.0	25	6	US-09-866-108-11912
C 11	12	80.0	25	6	US-09-866-108-11913
C 12	12	80.0	25	6	US-09-866-108-11914
C 13	12	80.0	25	6	US-09-866-108-11915
C 14	12	80.0	25	6	US-09-866-108-11916
C 15	12	80.0	25	6	US-09-866-108-11917
C 16	12	80.0	25	6	US-09-866-108-11918
C 17	12	80.0	25	6	US-09-866-108-11919
C 18	12	80.0	25	6	US-09-866-108-11920
C 19	12	80.0	25	6	US-09-866-108-11921
C 20	12	80.0	25	6	US-09-866-108-11922
C 21	11.8	78.7	27	7	US-09-772-315-2
C 22	11.8	78.7	38	5	US-09-371-772B-7807
C 23	11.8	78.7	38	5	US-09-708-690-10084
C 24	11.4	76.0	20	5	US-09-923-515-13
C 25	11.4	76.0	20	5	US-09-923-515-15

26	11.4	76.0	20	5	US-09-923-515-18	Sequence 18, Appl
27	11.4	76.0	20	6	US-09-198-452A-2269	Sequence 2269, Ap
28	11.4	76.0	20	6	US-09-198-452A-4764	Sequence 4764, Ap
29	11.4	76.0	47	5	US-09-877-804-10	Sequence 10, Appl
30	11	73.3	13	7	US-09-772-315-7	Sequence 7, Appl
31	11	73.3	17	6	US-09-866-108-7016	Sequence 7016, Ap
32	11	73.3	17	6	US-09-866-108-7023	Sequence 7023, Ap
33	11	73.3	20	1	PCT-US01-18763A-69	Sequence 69, Appl
34	11	73.3	20	1	PCT-US01-18763A-187	Sequence 187, App
35	11	73.3	22	1	PCT-US01-18763A-188	Sequence 188, App
36	11	73.3	22	7	US-09-772-315-12	Sequence 12, Appl
37	11	73.3	23	7	US-09-772-315-15	Sequence 15, Appl
38	11	73.3	25	6	US-09-866-108-11908	Sequence 11908, A
39	11	73.3	25	6	US-09-866-108-11923	Sequence 11923, A
40	11	73.3	28	5	US-09-766-095-12	Sequence 12, Appl
41	11	73.3	28	5	US-09-766-095-64	Sequence 64, Appl
42	11	73.3	28	5	US-09-766-095-78	Sequence 78, Appl
43	11	73.3	28	5	US-09-766-095-92	Sequence 92, Appl
44	11	73.3	45	6	US-09-728-792-7	Sequence 7, Appl
45	11	73.3	45	6	US-09-312-304B-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1
US-09-866-108-7017/c
; Sequence 7017, Application US/09866108
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOmica-7
; CURRENT APPLICATION NUMBER: US/09/866.108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: AeoMica Sequence Listing Engine
; SEQ ID NO 7017

;
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-7017

Query Match 80.0%; Score 12; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 aagcagctgccca 13
|||||
DB 17 AAGCAGCTGCCA 6

RESULT 2

US-09-866-108-7018/c
; Sequence 7018, Application US/09866108
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 7018
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-7018

Query Match 80.0%; Score 12; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 aagcagctgccca 13
|||||
DB 17 AAGCAGCTGCCA 6

QY 2 aagcagctgccca 13
|||||
DB 16 AAGCAGCTGCCA 5

RESULT 3

US-09-866-108-7019/c
; Sequence 7019, Application US/09866108
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 7019
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-7019

Query Match 80.0%; Score 12; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 aagcagctgccca 13
|||||
DB 15 AAGCAGCTGCCA 4

RESULT 4

US-09-866-108-7020/c
; Sequence 7020, Application US/09866108
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong


```
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 7020
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-7020

Query Match      80.0%; Score 12; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 aagcagctgtcca 13
        |||||
Db      14 AAGCAGCTGCCA 3

RESULT 5
US-09-866-108-7021/c
; Sequence 7021, Application US/09866108
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
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; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 7021
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-7021

Query Match      80.0%; Score 12; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 aagcagctgtcca 13
        |||||
Db      13 AAGCAGCTGCCA 2

RESULT 6
US-09-866-108-7022/c
; Sequence 7022, Application US/09866108
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
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; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Acomica Sequence Listing Engine
; SEQ ID NO 7022
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-7022

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```

Query Match      80.0%; Score 12; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 2 aagcagctgccca 13
    |||||
Db 12 AAGCAGCTGCCA 1

```

```

RESULT 7
US-09-866-108-11909/c
; Sequence 11909, Application US/09866108
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: ACOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30

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; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Acomica Sequence Listing Engine
; SEQ ID NO 11909
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-11909

```

```

Query Match      80.0%; Score 12; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 2 aagcagctgccca 13
    |||||
Db 25 AAGCAGCTGCCA 14

```

```

RESULT 8
US-09-866-108-11910/c
; Sequence 11910, Application US/09866108
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: ACOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05

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; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 11910
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-11910

Query Match 80.0%; Score 12; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 aagcagctgccca 13
| | | | | | | | | |
Db 24 AAGCAGCTGCCA 13

RESULT 9
US-09-866-108-11911/c
; Sequence 11911, Application US/09866108
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AECOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866.108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 11911
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-11911

Query Match 80.0%; Score 12; DB 6; Length 25;

Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 aagcagctgccca 13
| | | | | | | | | |
Db 23 AAGCAGCTGCCA 12

RESULT 10
US-09-866-108-11912/c
; Sequence 11912, Application US/09866108
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AECOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866.108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 11912
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-11912

Query Match 80.0%; Score 12; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 aagcagctgccca 13
| | | | | | | | | |
Db 22 AAGCAGCTGCCA 11

RESULT 11
US-09-866-108-11913/c

```
; Sequence 11913, Application US/09866108
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US 60/236,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 11913
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-11913
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```
Query Match      80.0%; Score 12; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 aagcagctgccca 13
Db      21 AAGCAGCTGCCA 10
|||||

RESULT 12
US-09-866-108-11914/c
; Sequence 11914, Application US/09866108
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
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; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 11914
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-11914

Query Match      80.0%; Score 12; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 aagcagctgccca 13
Db      20 AAGCAGCTGCCA 9
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RESULT 13
US-09-866-108-11915/c
; Sequence 11915, Application US/09866108
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
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; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 11917
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-11917

Query Match 80.0%; Score 12; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 aagcagctgccca 13
Db 17 AAGCAGCTGCCA 6

Search completed: October 2, 2001, 16:55:07
Job time: 17670 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: October 2, 2001, 21:50:19 ; Search time 17695.9 Seconds
(without alignments)
12.526 Million cell updates/sec

Title: US-09-757-100B-23

Perfect score: 15

Sequence: 1 gcgggctcacagtgg 15

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1415048 seqs, 7388405095 residues

Total number of hits satisfying chosen parameters: 4519004

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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55: /cgn2_6/ptodata/1/pna/US06023_COMB.seq:*

56: /cgn2_6/ptodata/1/pna/US06024_COMB.seq:*

57: /cgn2_6/ptodata/1/pna/US06025_COMB.seq:*

58: /cgn2_6/ptodata/1/pna/US06026_COMB.seq:*

59: /cgn2_6/ptodata/1/pna/US06027_COMB.seq:*

60: /cgn2_6/ptodata/1/pna/US06028_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	15	100.0	15	1	PCT-US000-18999-23
2	15	100.0	15	17	US-09-377-310-23
3	15	100.0	15	29	US-09-757-100B-23
4	15	100.0	20	1	PCT-US000-18999-3
5	15	100.0	20	17	US-09-377-310-3
6	15	100.0	20	29	US-09-757-100B-3
7	12.4	82.7	25	26	US-09-660-220-37375
8	12.4	82.7	25	26	US-09-660-220-37376
9	12.4	82.7	25	26	US-09-660-220-37377
10	12.4	82.7	25	55	US-60-232-638-136549
11	12.4	82.7	25	55	US-60-233-166-229423
12	12.4	82.7	25	55	US-60-233-166-296555
13	12.4	82.7	25	55	US-60-233-357-1753
14	12.4	82.7	25	55	US-60-234-017-297601
15	12	80.0	25	55	US-60-233-166-279728
16	12	80.0	25	55	US-60-233-166-386944
17	12	80.0	25	55	US-60-233-166-402639
18	11.8	78.7	21	7	US-08-778-052-157
19	11.8	78.7	21	7	US-08-339-207-89
20	11.8	78.7	24	15	US-09-177-306-52
21	11.8	78.7	25	55	US-60-233-166-185790
22	11.8	78.7	25	55	US-60-233-166-235736
23	11.8	78.7	25	55	US-60-234-017-10846
24	11.8	78.7	25	55	US-60-234-017-42928
25	11.8	78.7	25	55	US-60-234-017-55657
26	11.8	78.7	25	55	US-60-234-017-73527
27	11.8	78.7	25	55	US-60-234-017-273976
28	11.8	78.7	25	55	US-60-234-017-376806
29	11.8	78.7	25	55	US-60-234-017-376813
30	11.8	78.7	31	9	US-08-548-059-4
31	11.8	78.7	31	14	US-09-006-298-11
32	11.8	78.7	40	9	US-08-594-866-2
33	11.8	78.7	44	1	PCT-US000-00456-83
34	11.8	78.7	47	16	US-09-218-207-282
35	11.8	78.7	47	17	US-09-338-907-282
36	11.4	76.0	17	29	US-09-724-389-56
37	11.4	76.0	18	1	PCT-US99-16219-17
38	11.4	76.0	18	17	US-09-387-341-160
39	11.4	76.0	22	8	US-08-445-289-25
40	11.4	76.0	25	26	US-09-660-080-7306
41	11.4	76.0	25	26	US-09-660-220-14258
42	11.4	76.0	25	26	US-09-660-220-25361
43	11.4	76.0	25	26	US-09-660-220-68034
44	11.4	76.0	25	26	US-09-660-220-136997
45	11.4	76.0	25	55	US-60-234-049-78752

ALIGNMENTS

RESULT 1
PCT-US00-18999-23
; Sequence 23, Application PC/TUS0018999
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Monia, Brett P.
; APPLICANT: Gaarde, William A.
; APPLICANT: Nero, Pamela S.
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
; FILE REFERENCE: ISPH-0476
; CURRENT APPLICATION NUMBER: PCT/US00/18999
; PRIOR FILING DATE: 2000-07-13
; PRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
PCT-US00-18999-23

Query Match 100.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gcgggctcacagtgg 15
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Db 1 gcgggctcacagtgg 15

RESULT 2
US-09-377-310-23
; Sequence 23, Application US/09377310A
; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P.
; APPLICANT: Gaarde, William A.
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
; FILE REFERENCE: ISPH-0389
; CURRENT APPLICATION NUMBER: US/09/377,310A
; PRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
US-09-377-310-23

Query Match 100.0%; Score 15; DB 17; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gcgggctcacagtgg 15
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Db 1 gcgggctcacagtgg 15

RESULT 3
US-09-757-100B-23
; Sequence 23, Application US/09757100B

; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P.
; APPLICANT: Gaarde, William A.
; APPLICANT: Nero, Pamela S.
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
; FILE REFERENCE: ISPH-0533
; CURRENT APPLICATION NUMBER: US/09/757,100B
; CURRENT FILING DATE: 2001-03-15
; PRIOR FILING DATE: 1999-08-19
; PRIOR FILING DATE: 1999-08-19
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
US-09-757-100B-23

Query Match 100.0%; Score 15; DB 29; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gcgggctcacagtgg 15
| | | | | | | | | | | | | | |
Db 1 gcgggctcacagtgg 15

RESULT 4
PCT-US00-18999-3
; Sequence 3, Application PC/TUS0018999
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Monia, Brett P.
; APPLICANT: Gaarde, William A.
; APPLICANT: Nero, Pamela S.
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
; FILE REFERENCE: ISPH-0476
; CURRENT APPLICATION NUMBER: PCT/US00/18999
; CURRENT FILING DATE: 2000-07-13
; PRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
PCT-US00-18999-3

Query Match 100.0%; Score 15; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gcgggctcacagtgg 15
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Db 3 gcgggctcacagtgg 17

RESULT 5
US-09-377-310-3
; Sequence 3, Application US/09377310A
; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P.

; APPLICANT: Gaarde, William A.
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
; FILE OF INVENTION: Expression
; FILE REFERENCE: ISPH-0389
; CURRENT APPLICATION NUMBER: US/09/377,310A
; CURRENT FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
US-09-377-310-3

Query Match 100.0%; Score 15; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 3 gcgggctcacagtgg 17
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RESULT 6

US-09-757-100b-3
; Sequence 3, Application US/09757100B
; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P.
; APPLICANT: Gaarde, William A.
; APPLICANT: Nero, Pamela S.
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
; FILE OF INVENTION: Expression
; FILE REFERENCE: ISPH-0533
; CURRENT APPLICATION NUMBER: US/09/757,100B
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 09/377,310
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/US00/18999
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
US-09-757-100b-3

Query Match 100.0%; Score 15; DB 29; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gcgggctcacagtgg 15
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Db 3 gcgggctcacagtgg 17
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RESULT 7

US-09-660-220-37375
; Sequence 37375, Application US/09660220
; GENERAL INFORMATION:
; APPLICANT: Mittmann et al.
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of Human
; FILE REFERENCE: 3102.1
; CURRENT APPLICATION NUMBER: US/09/660,220
; CURRENT FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 60/164,973

; PRIOR FILING DATE: 1999-11-11
; NUMBER OF SEQ ID NOS: 140981
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 37375
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo Sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank L11931
US-09-660-220-37375

Query Match 82.7%; Score 12.4; DB 26; Length 25;
Best Local Similarity 92.9%; Pred. No. 1.1e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 cgggctcacagtgg 15
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Db 12 cgggctcacagtgg 25
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RESULT 8

US-09-660-220-37376
; Sequence 37376, Application US/09660220
; GENERAL INFORMATION:
; APPLICANT: Mittmann et al.
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of Human
; FILE REFERENCE: 3102.1
; CURRENT APPLICATION NUMBER: US/09/660,220
; CURRENT FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 60/164,973
; PRIOR FILING DATE: 1999-11-11
; NUMBER OF SEQ ID NOS: 140981
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 37376
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo Sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank L11931
US-09-660-220-37376

Query Match 82.7%; Score 12.4; DB 26; Length 25;
Best Local Similarity 92.9%; Pred. No. 1.1e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 cgggctcacagtgg 15
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Db 8 cgggctcacagtgg 21
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RESULT 9

US-09-660-220-37377
; Sequence 37377, Application US/09660220
; GENERAL INFORMATION:
; APPLICANT: Mittmann et al.
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of Human
; FILE REFERENCE: 3102.1
; CURRENT APPLICATION NUMBER: US/09/660,220
; CURRENT FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 60/164,973
; PRIOR FILING DATE: 1999-11-11
; NUMBER OF SEQ ID NOS: 140981
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 37377
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo Sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank L11931

US-09-660-220-37377

Query Match 82.7%; Score 12.4; DB 26; Length 25;
Best Local Similarity 92.9%; Pred. No. 1.1e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 cgggctcacagtgg 15
|||||

Db 4 cgggctcacagtgg 17

RESULT 10

US-60-232-638-136549/c
; Sequence 136549, Application US/60232638

; GENERAL INFORMATION:

; APPLICANT: Mitmann

; APPLICANT: Affymetrix, Inc.

; TITLE OF INVENTION: Methods of Genetic Analysis of Yeast

; FILE REFERENCE: 3110

; CURRENT APPLICATION NUMBER: US/60/232,638

; NUMBER OF SEQ ID NOS: 13810

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 136549

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Saccharomyces Cerevisiae

; PUBLICATION INFORMATION:

; DATABASE ACCESSION NUMBER: SGD YPR119W

US-60-232-638-136549

Query Match

82.7%; Score 12.4; DB 55; Length 25;

Best Local Similarity 92.9%; Pred. No. 1.1e+04;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 gcgggctcacagtgg 14

|||||

Db 20 GCGGCGCACACAGTG 7

RESULT 11

US-60-233-166-229423

; Sequence 229423, Application US/60233166

; GENERAL INFORMATION:

; APPLICANT: Mitmann

; APPLICANT: Affymetrix, Inc.

; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat

; FILE REFERENCE: 3112

; CURRENT APPLICATION NUMBER: US/60/233,166

; NUMBER OF SEQ ID NOS: 2000-10-24

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 229423

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Rattus norvegicus

; PUBLICATION INFORMATION:

; DATABASE ACCESSION NUMBER: GenBank AF016901

US-60-233-166-229423

Query Match

82.7%; Score 12.4; DB 55; Length 25;

Best Local Similarity 92.9%; Pred. No. 1.1e+04;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 cgggctcacagtgg 15

|||||

Db 1 cgggctcacagtgg 14

RESULT 12

US-60-233-166-296555/c

; Sequence 296555, Application US/60233166

; GENERAL INFORMATION:

; APPLICANT: Mitmann

; APPLICANT: Affymetrix, Inc.

; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat

; FILE REFERENCE: 3112

; CURRENT APPLICATION NUMBER: US/60/233,166

; CURRENT FILING DATE: 2000-10-24

; NUMBER OF SEQ ID NOS: 420907

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 296555

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Rattus norvegicus

; PUBLICATION INFORMATION:

; DATABASE ACCESSION NUMBER: GenBank AF016901

US-60-233-166-296555

Query Match

82.7%; Score 12.4; DB 55; Length 25;

Best Local Similarity 92.9%; Pred. No. 1.1e+04;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 cgggctcacagtgg 15

|||||

Db 23 GCGGCGCACAGTGG 10

RESULT 13

US-60-233-357-1753

; Sequence 1753, Application US/60233357

; GENERAL INFORMATION:

; APPLICANT: Mitmann

; APPLICANT: Affymetrix, Inc.

; TITLE OF INVENTION: Methods of Genetic Analysis of Rat

; FILE REFERENCE: 3114

; CURRENT APPLICATION NUMBER: US/60/233,357

; CURRENT FILING DATE: 2000-10-24

; NUMBER OF SEQ ID NOS: 21305

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 1753

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Rattus norvegicus

; PUBLICATION INFORMATION:

; DATABASE ACCESSION NUMBER: GenBank AF016901

US-60-233-357-1753

Query Match

82.7%; Score 12.4; DB 55; Length 25;

Best Local Similarity 92.9%; Pred. No. 1.1e+04;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 cgggctcacagtgg 15

|||||

Db 1 cgggctcacagtgg 14

RESULT 14

US-60-234-017-297601/c

; Sequence 297601, Application US/60234017

; GENERAL INFORMATION:

; APPLICANT: Mitmann, M

; APPLICANT: Affymetrix, Inc.

; TITLE OF INVENTION: Methods of Genetic Analysis of Mus

; FILE REFERENCE: 3115

; CURRENT APPLICATION NUMBER: US/60/234,017

; CURRENT FILING DATE: 2000-09-20

; NUMBER OF SEQ ID NOS: 605887
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 297601
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank AI854291
US-60-234-017-297601

Query Match 82.7%; Score 12.4; DB 55; Length 25;
Best Local Similarity 92.9%; Pred. No. 1.1e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 cgggctcacagtgg 15
||| |||||
Db 20 CGGACTCACAGTGG 7

RESULT 15
US-60-233-166-279728/c
; Sequence 279728, Application US/60233166
; GENERAL INFORMATION:
; APPLICANT: Mittmann
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat
; TITLE OF INVENTION: Genome
; FILE REFERENCE: 3112
; CURRENT APPLICATION NUMBER: US/60/233,166
; CURRENT FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 420907
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 279728
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank AI639107
US-60-233-166-279728

Query Match 80.0%; Score 12; DB 55; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ggctcacagtgg 15
||| |||||
Db 21 GGCTCACAGTGG 10

Search completed: October 2, 2001, 21:50:20
Job time: 24533 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 2, 2001, 16:55:06 ; Search time 2173.58 Seconds
(without alignments)
14.467 Million cell updates/sec

Title: US-09-757-100B-23

Perfect score: 15

Sequence: 1 gcgggtcacagtgg 15

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1895189 seqs, 1048201267 residues

Total number of hits satisfying chosen parameters: 299022

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending_Patents_NA_New.*

- 1: /cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq.*
- 2: /cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq.*
- 3: /cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq.*
- 4: /cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq.*
- 5: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq.*
- 6: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq1.*
- 7: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq2.*
- 8: /cgn2_6/ptodata/2/pna/US60_NEW_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
c 1	11.4	76.0	18	7 US-09-787-252-17	Sequence 17, Appl
2	11.4	76.0	25	7 US-09-735-271-2037	Sequence 2037, Ap
c 3	11.4	76.0	40	7 US-09-735-271-1558	Sequence 1558, Ap
4	10.4	69.3	17	6 US-09-866-108-10732	Sequence 10732, A
5	10.4	69.3	17	6 US-09-866-108-10733	Sequence 10733, A
6	10.4	69.3	17	6 US-09-866-108-10734	Sequence 10734, A
7	10.4	69.3	17	6 US-09-866-108-10735	Sequence 10735, A
8	10.4	69.3	17	6 US-09-866-108-10736	Sequence 10736, A
9	10.4	69.3	17	6 US-09-866-108-10737	Sequence 10737, A
c 10	10.4	69.3	18	5 US-09-925-548-93	Sequence 93, Appl
11	10.4	69.3	20	5 US-09-827-383-1980	Sequence 1980, Ap
c 12	10.4	69.3	21	6 US-09-765-081-1111	Sequence 111, App
13	10.4	69.3	25	6 US-09-866-108-15624	Sequence 15624, A
14	10.4	69.3	25	6 US-09-866-108-15625	Sequence 15625, A
15	10.4	69.3	25	6 US-09-866-108-15626	Sequence 15626, A
16	10.4	69.3	25	6 US-09-866-108-15627	Sequence 15627, A
17	10.4	69.3	25	6 US-09-866-108-15628	Sequence 15628, A
18	10.4	69.3	25	6 US-09-866-108-15629	Sequence 15629, A
19	10.4	69.3	25	6 US-09-866-108-15630	Sequence 15630, A
20	10.4	69.3	25	6 US-09-866-108-15631	Sequence 15631, A
21	10.4	69.3	25	6 US-09-866-108-15632	Sequence 15632, A
22	10.4	69.3	25	6 US-09-866-108-15633	Sequence 15633, A
23	10.4	69.3	25	6 US-09-866-108-15634	Sequence 15634, A
24	10.4	69.3	25	6 US-09-866-108-15635	Sequence 15635, A
25	10.4	69.3	25	6 US-09-866-108-15636	Sequence 15636, A

26	10.4	69.3	25	6 US-09-866-108-15637	Sequence 15637, A
27	10.4	69.3	29	7 US-09-735-271-1792	Sequence 1792, Ap
28	10.4	69.3	31	6 US-09-801-274-629	Sequence 629, App
29	10.4	69.3	36	5 US-09-245-026-21	Sequence 21, Appl
30	10.4	69.3	36	6 US-09-245-025-21	Sequence 21, Appl
c 31	10.4	69.3	37	5 US-09-708-690-20444	Sequence 20444, A
32	10.4	69.3	48	7 US-09-864-785-3509	Sequence 3509, Ap
c 33	10.2	68.0	17	5 US-09-708-690-9309	Sequence 9309, Ap
34	10.2	68.0	17	6 US-09-866-108-2229	Sequence 2229, Ap
35	10.2	68.0	17	6 US-09-866-108-2230	Sequence 2230, Ap
36	10.2	68.0	17	6 US-09-866-108-2231	Sequence 2231, Ap
37	10.2	68.0	20	7 US-09-825-497-23	Sequence 23, Appl
38	10.2	68.0	25	6 US-09-879-341-12	Sequence 12, Appl
39	10.2	68.0	25	6 US-09-866-108-5158	Sequence 5158, Ap
40	10.2	68.0	25	6 US-09-866-108-5159	Sequence 5159, Ap
41	10.2	68.0	25	6 US-09-866-108-5160	Sequence 5160, Ap
42	10.2	68.0	25	6 US-09-866-108-5161	Sequence 5161, Ap
43	10.2	68.0	25	6 US-09-866-108-5162	Sequence 5162, Ap
44	10.2	68.0	25	6 US-09-866-108-5163	Sequence 5163, Ap
45	10.2	68.0	25	6 US-09-866-108-5164	Sequence 5164, Ap

ALIGNMENTS

RESULT 1
US-09-787-252-17/c
; Sequence 17, Application US/09787252
; GENERAL INFORMATION:
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF RHO G EXPRESSION
; FILE REFERENCE: RTSP-Q106
; CURRENT APPLICATION NUMBER: US/09/787,252
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 09/161,015
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 17
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-787-252-17

Query Match	76.0%	Score 11.4;	DB 7;	Length 18;
Best Local Similarity	92.3%	Pred. No. 5.2e+03;		
Matches 12;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
Oy 2	cggggtcacagtgg 14			
Db 17	CGGGCGCACAGTG 5			
RESULT 2				
US-09-735-271-2037				
; Sequence 2037, Application US/09735271				
; GENERAL INFORMATION:				
; APPLICANT: Daly, Mark J.				
; APPLICANT: Hudson, Thomas J.				
; APPLICANT: Lander, Eric S.				
; APPLICANT: Rioux, John				
; APPLICANT: Siminovitch, Kathy				
; TITLE OF INVENTION: IBD-RELATED POLYMORPHISMS				
; FILE REFERENCE: 2825.1025-002				
; CURRENT APPLICATION NUMBER: US/09/735,271				
; CURRENT FILING DATE: 2000-12-11				
; PRIOR APPLICATION NUMBER: US 60/170,257				
; PRIOR FILING DATE: 1999-12-10				
; PRIOR APPLICATION NUMBER: US 60/196,046				
; PRIOR FILING DATE: 2000-04-10				
; NUMBER OF SEQ ID NOS: 2058				

```
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2037
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-735-271-2037
```

```
Query Match          76.0%; Score 11.4; DB 7; Length 25;
Best Local Similarity 92.3%; Pred. No. 5.3e+03;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 2 cggggtcacagt 14
    ||| ||||| |||
Db 4 cgggtcacagt 16
```

```
RESULT 3
US-09-735-271-1558/c
; Sequence 1558, Application US/09735271
; GENERAL INFORMATION:
; APPLICANT: Daly, Mark J.
; APPLICANT: Hudson, Thomas J.
; APPLICANT: Lander, Eric S.
; APPLICANT: Rioux, John
; APPLICANT: Siminovich, Kathy
; TITLE OF INVENTION: IBD-RELATED POLYMORPHISMS
; FILE REFERENCE: 2825.1025-002
; CURRENT APPLICATION NUMBER: US/09/735,271
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 60/170,257
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 60/196,046
; PRIOR FILING DATE: 2000-04-10
; NUMBER OF SEQ ID NOS: 2058
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1558
; LENGTH: 40
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(40)
; OTHER INFORMATION: n = A,T,C or G
US-09-735-271-1558
```

```
Query Match          76.0%; Score 11.4; DB 7; Length 40;
Best Local Similarity 92.3%; Pred. No. 5.5e+03;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 1 gcggggtcacagt 13
    |||| | |||||
Db 35 GCGGGGTCACT 23
```

```
RESULT 4
US-09-866-108-10732
; Sequence 10732, Application US/09866108
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MTOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
```

```
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 10732
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-10732
```

```
Query Match          69.3%; Score 10.4; DB 6; Length 17;
Best Local Similarity 91.7%; Pred. No. 2e+04;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 3 ggggtcacagt 14
    ||||| |||||
Db 6 ggggtcacagt 17
```

```
RESULT 5
US-09-866-108-10733
; Sequence 10733, Application US/09866108
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
```

; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 10733
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-10733

Query Match 69.3%; Score 10.4; DB 6; Length 17;
Best Local Similarity 91.7%; Pred. No. 2e+04;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 gggtccacagt 14
|||||
Db 5 gggtccacagt 16

RESULT 6
US-09-866-108-10734
; Sequence 10734, Application US/09866108
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 10733

; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 10734
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-10734

Query Match 69.3%; Score 10.4; DB 6; Length 17;
Best Local Similarity 91.7%; Pred. No. 2e+04;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 gggtccacagt 14
|||||
Db 4 gggtccacagt 15

RESULT 7
US-09-866-108-10735
; Sequence 10735, Application US/09866108
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine

; APPLICANT: Dedhar, Shoukat
; APPLICANT: Hannigan, Greg
; APPLICANT: Yee, Arthur
; TITLE OF INVENTION: INTEGRIN-LINKED KINASE AND ITS USES
; FILE REFERENCE: KINE001CIP4
; CURRENT APPLICATION NUMBER: US/09/925,548
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 09/390,425
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: 09/035,706
; PRIOR FILING DATE: 1998-03-05
; PRIOR APPLICATION NUMBER: 08/955,841
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 08/752,345
; PRIOR FILING DATE: 1996-11-19
; PRIOR APPLICATION NUMBER: 60/009,074
; PRIOR FILING DATE: 1995-12-21
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 93
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-548-93

Query Match 69.3%; Score 10.4; DB 5; Length 18;
Best Local Similarity 91.7%; Pred. No. 2e+04;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 qcgggctcacag 12
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Db 13 GCGGGCTCAGAG 2

RESULT 11
US-09-827-383-1980
; Sequence 1980, Application US/09827383
; GENERAL INFORMATION:
; APPLICANT: Michael Wittmann
; APPLICANT: Macdonald Morris
; APPLICANT: Tom Ryder
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Tag Nucleic Acids and Probe Arrays
; FILE REFERENCE: 3108
; CURRENT APPLICATION NUMBER: US/09/827,383
; CURRENT FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: US 60/195,585
; PRIOR FILING DATE: 2000-04-06
; NUMBER OF SEQ ID NOS: 2050
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1980
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-383-1980

Query Match 69.3%; Score 10.4; DB 5; Length 20;
Best Local Similarity 91.7%; Pred. No. 2e+04;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 cgggctcacagt 13
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Db 2 cgggctcaagt 13

RESULT 12
US-09-765-081-111/c
; Sequence 111, Application US/09765081
; GENERAL INFORMATION:
; APPLICANT: Cargill, Michele

; APPLICANT: Ireland, James S.
; APPLICANT: Lander, Eric S.
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: 2825.2008-001
; CURRENT APPLICATION NUMBER: US/09/765,081
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,861
; PRIOR FILING DATE: 2000-01-19
; NUMBER OF SEQ ID NOS: 461
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 111
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-765-081-111

Query Match 69.3%; Score 10.4; DB 6; Length 21;
Best Local Similarity 78.6%; Pred. No. 2e+04;
Matches 11; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 cgggctcacagtgg 15
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Db 15 CGGASTCACAGTTG 2

RESULT 13
US-09-866-108-15624
; Sequence 15624, Application US/09866108
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
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; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine

; SEQ ID NO 15624
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-15624

Query Match 69.3%; Score 10.4; DB 6; Length 25;
Best Local Similarity 91.7%; Pred. No. 2e+04;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 gggctccacagt 14
||||| |||||
Db 14 gggctccacagt 25

RESULT 14
US-09-866-108-15625
; Sequence 15625, Application US/09866108
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
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; PRIOR APPLICATION NUMBER: PCT/US01/00669
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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 15625
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-15625

Query Match 69.3%; Score 10.4; DB 6; Length 25;
Best Local Similarity 91.7%; Pred. No. 2e+04;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 gggctccacagt 14
||||| |||||
Db 13 gggctccacagt 24

RESULT 15
US-09-866-108-15626
; Sequence 15626, Application US/09866108
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
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; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 15626
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-15626

Query Match 69.3%; Score 10.4; DB 6; Length 25;
Best Local Similarity 91.7%; Pred. No. 2e+04;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 gggctccacagt 14
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Db 12 gggctccacagt 23

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OM nucleic - nucleic search, using sw model

Run on: October 2, 2001, 21:50:18 ; Search time 17695.9 Seconds
(without alignments)
16.701 Million cell updates/sec

Title: US-09-757-100B-20

Perfect score: 20
Sequence: 1 catgatgcttaaaagcttac 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 14155048 seqs, 7388405095 residues

Total number of hits satisfying chosen parameters: 4519004

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	20	100.0	20	1	PCT-US00-18999-20
2	20	100.0	20	17	US-09-377-310-20
3	20	100.0	20	29	US-09-757-100B-20
4	15	75.0	15	1	PCT-US00-18999-40
5	15	75.0	15	17	US-09-377-310-40
6	15	75.0	15	29	US-09-757-100B-40
7	14.2	71.0	25	55	US-60-234-017-498317
8	13.8	69.0	27	16	US-09-261-301C-8
9	13.6	68.0	25	55	US-60-233-166-44325
10	13.6	68.0	25	55	US-60-233-620-123801
11	13.6	68.0	25	55	US-60-234-017-564512
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13	13.6	68.0	25	55	US-60-234-017-564524
14	13.6	68.0	25	55	US-60-234-017-564527
15	13.4	67.0	25	55	US-60-232-638-137320
16	13.4	67.0	25	55	US-60-232-638-137321
17	13.4	67.0	25	55	US-60-234-017-394023
18	13.4	67.0	44	12	US-08-818-604A-5
19	13.2	66.0	22	17	US-09-345-828-8
20	13.2	66.0	25	55	US-60-232-638-82143
21	13.2	66.0	33	6	US-08-224-593-5
22	13.2	66.0	33	19	US-09-509-668-4
23	13.2	66.0	48	55	US-60-234-690-4034
24	13	65.0	25	55	US-60-232-638-68442
25	12.8	64.0	25	55	US-60-232-638-6612
26	12.8	64.0	25	55	US-60-232-638-6621
27	12.8	64.0	25	55	US-60-232-638-6632
28	12.8	64.0	25	55	US-60-233-620-46459
29	12.8	64.0	25	55	US-60-233-620-82138
30	12.8	64.0	25	55	US-60-233-620-82143
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ALIGNMENTS

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RESULT 1
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; Sequence 20, Application PC/TUS0018999
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Monia, Brett P.
; APPLICANT: Gaarde, William A.
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
; FILE REFERENCE: ISPH-0476
; CURRENT APPLICATION NUMBER: PCT/US00/18999
; PRIOR FILING DATE: 2000-07-13
; PRIOR APPLICATION NUMBER: 09/377,310
; PRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
PCT-US00-18999-20

Query Match 100.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 catgatgcttaaaagcttac 20
Db 1 catgatgcttaaaagcttac 20
|||||

RESULT 2
US-09-377-310-20
; Sequence 20, Application US/09377310A
; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P.
; APPLICANT: Gaarde, William A.
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
; FILE REFERENCE: ISPH-0389
; CURRENT APPLICATION NUMBER: US/09/377,310A
; PRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
US-09-377-310-20

Query Match 100.0%; Score 20; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 catgatgcttaaaagcttac 20
Db 1 catgatgcttaaaagcttac 20
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RESULT 3
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; Sequence 20, Application US/09757100B
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; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P.
; APPLICANT: Gaarde, William A.
; APPLICANT: Nero, Pamela S.
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
; FILE REFERENCE: ISPH-0533
; CURRENT APPLICATION NUMBER: US/09/757,100B
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 09/377,310
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/US00/18999
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.0
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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
US-09-757-100B-20
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Query Match 100.0%; Score 20; DB 29; Length 20;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 catgatgcttaaaagcttac 20
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RESULT 4
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; Sequence 40, Application PC/TUS0018999
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Monia, Brett P.
; APPLICANT: Gaarde, William A.
; APPLICANT: Nero, Pamela S.
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
; FILE REFERENCE: ISPH-0476
; CURRENT APPLICATION NUMBER: PCT/US00/18999
; CURRENT FILING DATE: 2000-07-13
; PRIOR APPLICATION NUMBER: 09/377,310
; PRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
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; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
PCT-US00-18999-40
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Query Match 75.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 tgatgcttaaaagct 15
|||||
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RESULT 5
US-09-377-310-40
; Sequence 40, Application US/09377310A
; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P.
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; APPLICANT: Gaarde, William A.
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
; FILE REFERENCE: ISPH-0389
; CURRENT APPLICATION NUMBER: US/09/377,310A
; CURRENT FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 40
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
US-09-377-310-40

Query Match 75.0%; Score 15; DB 17; Length 15;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 tgatgcttaaaagct 17
|||||

Db 1 tgatgcttaaaagct 15

RESULT 6

US-09-757-100B-40

; Sequence 40, Application US/09757100B
; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P.
; APPLICANT: Gaarde, William A.
; APPLICANT: Nero, Pamela S.
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
; FILE REFERENCE: ISPH-0533
; CURRENT APPLICATION NUMBER: US/09/757,100B
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 09/377,310
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/US00/18999
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 40
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence

US-09-757-100B-40

Query Match 75.0%; Score 15; DB 29; Length 15;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 tgatgcttaaaagct 17
|||||

Db 1 tgatgcttaaaagct 15

RESULT 7

US-60-234-017-498317

; Sequence 498317, Application US/60234017
; GENERAL INFORMATION:
; APPLICANT: Mittmann, M
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of Mus
; FILE REFERENCE: 3115
; CURRENT APPLICATION NUMBER: US/60/234,017
; CURRENT FILING DATE: 2000-09-20

; NUMBER OF SEQ ID NOS: 605887
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 498317
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank AV213434
US-60-234-017-498317

Query Match 71.0%; Score 14.2; DB 55; Length 25;
Best Local Similarity 84.2%; Pred. No. 8e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 atgatgcttaaaagcttac 20
|||

Db 7 atactgcttaaaagtttac 25

RESULT 8

US-09-261-301C-8/C

; Sequence 8, Application US/09261301C
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Aharonowitz, Yair
; APPLICANT: Borovok, Ilya
; APPLICANT: Cohen, Gerald
; APPLICANT: *Uziel, Orit
; TITLE OF INVENTION: Recombinant Staphylococcus
; TITLE OF INVENTION: Thiorodoxin Reductase, And Inhibitors
; TITLE OF INVENTION: Thereof Useful As Antimicrobial Agents
; FILE REFERENCE: 6286.US.01
; CURRENT APPLICATION NUMBER: US/09/261,301C
; CURRENT FILING DATE: 1999-03-02
; PRIOR APPLICATION NUMBER: US 60/076,525
; PRIOR FILING DATE: 1998-03-02
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 27
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: C-terminal primer

US-09-261-301C-8

Query Match 69.0%; Score 13.8; DB 16; Length 27;
Best Local Similarity 88.2%; Pred. No. 1.3e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 atgatgcttaaaagctt 18
|||

Db 20 ATCAAGCTTAAAGCTT 4

RESULT 9

US-60-233-166-44325

; Sequence 44325, Application US/60233166
; GENERAL INFORMATION:
; APPLICANT: Mittmann
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat
; FILE REFERENCE: 3112
; CURRENT APPLICATION NUMBER: US/60/233,166
; CURRENT FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 420907
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 44325
; LENGTH: 25

Query Match 68.0%; Score 13.6; DB 55; Length 25;
Best Local Similarity 80.0%; Pred. No. 1.6e+04;
Matches 16; Conservative 0; Mismatches 4; Indels

; TITLE OF INVENTION: Methods of Genetic Analysis of Mus

; FILE OF INVENTION: musculus

; FILE REFERENCE: 3115

; CURRENT APPLICATION NUMBER: US/60/234,017

; CURRENT FILING DATE: 2000-09-20

; NUMBER OF SEQ ID NOS: 605887

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 564527

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Mus musculus

; PUBLICATION INFORMATION:

; DATABASE ACCESSION NUMBER: GenBank AV245764

US-60-234-017-564527

Query Match 68.0%; Score 13.6; DB 55; Length 25;

Best Local Similarity 80.0%; Pred. No. 1.6e+04;

Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 catgatgcttaaaagcttac 20

||||| || ||| |||||

Db 24 CAAGATGATTGAGGCTTAC 5

RESULT 15

US-60-232-638-137320/c

; Sequence 137320. Application US/60232638

; GENERAL INFORMATION:

; APPLICANT: Mitmann

; APPLICANT: Affymetrix, Inc.

; TITLE OF INVENTION: Methods of Genetic Analysis of Yeast

; FILE REFERENCE: 3110

; CURRENT APPLICATION NUMBER: US/60/232,638

; CURRENT FILING DATE: 2000-09-14

; NUMBER OF SEQ ID NOS: 138410

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 137320

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Saccharomyces Cerevisiae

; PUBLICATION INFORMATION:

; DATABASE ACCESSION NUMBER: SGD YPR165W

US-60-232-638-137320

Query Match 67.0%; Score 13.4; DB 55; Length 25;

Best Local Similarity 93.3%; Pred. No. 2e+04;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 atgatgcttaaaagc 16

||||| ||| |||||

Db 21 ATGATGCTTACAGC 7

Search completed: October 2, 2001, 21:50:19

Job time: 24532 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 2, 2001, 16:55:06 ; Search time 2173.58 Seconds
(without alignments)
19.290 Million cell updates/sec

Title: US-09-757-100B-20

Perfect score: 20

Sequence: 1 catgatgcttaaaagcttac 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1895189 seqs, 1048201267 residues

Total number of hits satisfying chosen parameters: 299022

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Pending_Patents_NA_New.*
1: /cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq.*
2: /cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq.*
3: /cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq.*
4: /cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq.*
5: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq.*
6: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq1.*
7: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq2.*
8: /cgn2_6/ptodata/2/pna/US60_NEW_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
c 1	12.8	64.0	21	6	US-09-715-849-159
c 2	12.6	63.0	36	5	US-09-536-784-418
c 3	12.6	63.0	36	6	US-09-765-272-418
c 4	12.2	61.0	33	5	US-09-536-784-330
c 5	12.2	61.0	33	6	US-09-765-272-330
c 6	12.2	61.0	41	8	US-60-253-378-31544
c 7	12.2	61.0	47	8	US-60-295-722-6
c 8	12.2	61.0	47	8	US-60-295-600-6
c 9	12.2	61.0	47	8	US-60-295-722-6
c 10	12.2	61.0	20	5	US-09-923-515-39
c 11	12.2	60.0	31	5	US-09-536-784-272
c 12	12.2	60.0	31	6	US-09-765-272-272
c 13	12.2	60.0	34	5	US-09-536-784-316
c 14	12.2	60.0	34	6	US-09-765-272-316
c 15	11.8	59.0	37	7	US-09-591-306-33
c 16	11.6	58.0	18	8	US-60-301-889-40
c 17	11.6	58.0	26	5	US-09-310-735A-328
c 18	11.6	58.0	26	5	US-09-310-735A-346
c 19	11.6	58.0	26	5	US-09-310-844B-328
c 20	11.6	58.0	26	5	US-09-310-844B-346
c 21	11.6	58.0	40	8	US-60-301-889-41
c 22	11.6	58.0	42	7	US-09-840-424-747
c 23	11.6	58.0	48	5	US-09-554-341-5
c 24	11.6	58.0	50	8	US-60-252-833-36224
c 25	11.6	58.0	50	8	US-60-253-456-6918

ALIGNMENTS

RESULT 1

US-09-715-849-159/c

; Sequence 159, Application US/09715849

; GENERAL INFORMATION:

; APPLICANT: Cargill, Michele

; APPLICANT: Ireland, James S.

; APPLICANT: Lander, Eric S.

; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS

; FILE REFERENCE: 2825.2002-001

; CURRENT APPLICATION NUMBER: US/09/715.849

; CURRENT FILING DATE: 2000-11-17

; PRIOR APPLICATION NUMBER: US 60/167,334

; PRIOR FILING DATE: 1999-11-24

; NUMBER OF SEQ ID NOS: 589

; SOFTWARE: FASTSEQ for Windows Version 4.0

; SEQ ID NO 159

; LENGTH: 21

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-715-849-159

Query Match 64.0%; Score 12.8; DB 6; Length 21;

Best Local Similarity 77.8%; Pred. No. 4.3e+03;

Matches 14; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 catgatgcttaaaagctt 18

||| ||| : |||||

Db 18 CATAATYTAAGCTT 1

RESULT 2

US-09-536-784-418/c

; Sequence 418, Application US/09536784

; GENERAL INFORMATION:

; APPLICANT: Choi et. al.

; TITLE OF INVENTION: Streptococcus pneumoniae Antigen and Vaccines

; NUMBER OF SEQUENCES: 452

; CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue

CITY: Rockville

STATE: Maryland

COUNTRY: USA

ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage

COMPUTER: HP Vectra 486/33

Sequence 15, Appl
Sequence 1852, Ap
Sequence 1853, Ap
Sequence 2491, Ap
Sequence 70, Appl
Sequence 66, Appl
Sequence 6, Appl
Sequence 118, App
Sequence 35, Appl
Sequence 18, Appl
Sequence 787, App
Sequence 1514, Ap
Sequence 15, Appl
Sequence 15, Appl
Sequence 28591, A
Sequence 345, App
Sequence 4, Appl
Sequence 39, Appl
Sequence 40, Appl

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;
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/536,784
; FILING DATE: 30-Oct-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/961,083
; FILING DATE: OCT-30-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Michelle S. Marks
; REGISTRATION NUMBER: 41,971
; REFERENCE/DOCKET NUMBER: PB340P3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 418:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 418:
US-09-536-784-418

Query Match 63.0%; Score 12.6; DB 5; Length 36;
Best Local Similarity 78.9%; Pred. No. 5.8e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 atgatgcttaaaagcttac 20
   || || | | | || || || |
Db 21 ATTATGTTGATAAGCTTAC 3

RESULT 3
US-09-765-272-418/c
; Sequence 418, Application US/09765272
; GENERAL INFORMATION:
; APPLICANT: Choi et. al.
; TITLE OF INVENTION: Streptococcus pneumoniae Antigen and Vaccines
; NUMBER OF SEQUENCES: 452
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/765,272
; FILING DATE: 22-Jan-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/961,083
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB340P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 418:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
```

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;
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 418:
US-09-765-272-418

Query Match 63.0%; Score 12.6; DB 6; Length 36;
Best Local Similarity 78.9%; Pred. No. 5.8e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 atgatgcttaaaagcttac 20
   || || | | | || || || |
Db 21 ATTATGTTGATAAGCTTAC 3

RESULT 4
US-09-536-784-330/c
; Sequence 330, Application US/09536784
; GENERAL INFORMATION:
; APPLICANT: Choi et. al.
; TITLE OF INVENTION: Streptococcus pneumoniae Antigen and Vaccines
; NUMBER OF SEQUENCES: 452
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/536,784
; FILING DATE: 30-Oct-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/961,083
; FILING DATE: OCT-30-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Michelle S. Marks
; REGISTRATION NUMBER: 41,971
; REFERENCE/DOCKET NUMBER: PB340P3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 330:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 330:
US-09-536-784-330

Query Match 61.0%; Score 12.2; DB 5; Length 33;
Best Local Similarity 82.4%; Pred. No. 9.1e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 gatgcttaaaagcttac 20
   || || | | | || || || |
Db 19 GAAGCTAATAAGCTTAC 3

RESULT 5
US-09-765-272-330/c
; Sequence 330, Application US/09765272
; GENERAL INFORMATION:
; APPLICANT: Choi et. al.
; TITLE OF INVENTION: Streptococcus pneumoniae Antigen and Vaccines
; NUMBER OF SEQUENCES: 452
```


; APPLICANT: Blake Denison
; APPLICANT: Frances Yen
; APPLICANT: Bernard Bihain
; APPLICANT: Lydie Bouquellet
; TITLE OF INVENTION: GSP4 Polynucleotides and Polypeptides and Uses Thereof
; FILE REFERENCE: 103.052.PRO
; CURRENT APPLICATION NUMBER: US/60/295,722
; CURRENT FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patent.pm
; SEQ ID NO 6
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-295-722-6

Query Match 61.0%; Score 12.2; DB 8; Length 47;
Best Local Similarity 82.4%; Pred. No. 9.6e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 4 gatgcttaaaagcttac 20
Db 23 GAAGTTTATAAGCTTAC 7

RESULT 10
US-09-923-515-39
; Sequence 39, Application US/09923515
; GENERAL INFORMATION:
; APPLICANT: Rosanne M. Crooke
; APPLICANT: Mark J. Graham
; TITLE OF INVENTION: ANTISENSE MODULATION OF APOLIPOPROTEIN(A) EXPRESSION
; FILE REFERENCE: ISPH-0595
; CURRENT APPLICATION NUMBER: US/09/923,515
; CURRENT FILING DATE: 2001-08-07
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 39
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-923-515-39

Query Match 60.0%; Score 12; DB 5; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 8 cttaaaagctta 19
Db 3 cttaaaagctta 14

RESULT 11
US-09-536-784-272/c
; Sequence 272, Application US/09536784
; GENERAL INFORMATION:
; APPLICANT: Choi et. al.
; TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
; NUMBER OF SEQUENCES: 452
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33

; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/536,784
; FILING DATE: 30-Oct-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/961,083
; FILING DATE: OCT-30-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Michelle S. Marks
; REGISTRATION NUMBER: 41,971
; REFERENCE/DOCKET NUMBER: PB340P3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 272:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 272:
US-09-536-784-272

Query Match 60.0%; Score 12; DB 5; Length 31;
Best Local Similarity 75.0%; Pred. No. 1.1e+04;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 1 catgatgcttaaaagcttac 20
Db 22 CATACTGCAGATAAGCTTAC 3

RESULT 12
US-09-765-272-272/c
; Sequence 272, Application US/09765272
; GENERAL INFORMATION:
; APPLICANT: Choi et. al.
; TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
; NUMBER OF SEQUENCES: 452
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/765,272
; FILING DATE: 22-Jan-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/961,083
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB340P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 272:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double

```
;
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 272:
US-09-765-272-272

Query Match          60.0%; Score 12; DB 6; Length 31;
Best Local Similarity 75.0%; Pred. No. 1.1e+04;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 catgatgcttaaaagcttac 20
   ||| ||| | |||||
Db 22 CATACTGCAGATAAGCTTAC 3

RESULT 13
US-09-536-784-316/c
; Sequence 316, Application US/09536784
; GENERAL INFORMATION:
; APPLICANT: Choi et. al.
; TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
; NUMBER OF SEQUENCES: 452
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/536,784
; FILING DATE: 30-Oct-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/961,083
; FILING DATE: OCT-30-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Michelle S. Marks
; REGISTRATION NUMBER: 41,971
; REFERENCE/DOCKET NUMBER: PB340p3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 316:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 316:
US-09-536-784-316

Query Match          60.0%; Score 12; DB 5; Length 34;
Best Local Similarity 75.0%; Pred. No. 1.1e+04;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 catgatgcttaaaagcttac 20
   ||| ||| | |||||
Db 22 CATACTGCAGATAAGCTTAC 3

RESULT 14
US-09-765-272-316/c
; Sequence 316, Application US/09765272
; GENERAL INFORMATION:
; APPLICANT: Choi et. al.
; TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
; NUMBER OF SEQUENCES: 452
```

```
;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/765,272
; FILING DATE: 22-Jan-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/961,083
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB340p2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 316:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 316:
US-09-765-272-316

Query Match          60.0%; Score 12; DB 6; Length 34;
Best Local Similarity 75.0%; Pred. No. 1.1e+04;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 catgatgcttaaaagcttac 20
   ||| ||| | |||||
Db 22 CCTACTGATTATAAGCTTAC 3

RESULT 15
US-09-591-306-33
; Sequence 33, Application US/09591306
; GENERAL INFORMATION:
; APPLICANT: Massachusetts general Hospital
; TITLE OF INVENTION: Novel transcription factor and uses therefor
; FILE REFERENCE: 17633/1170
; CURRENT APPLICATION NUMBER: US/09/591,306
; CURRENT FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: US 08/751,344
; PRIOR FILING DATE: 1996-11-19
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 33
; LENGTH: 37
; TYPE: DNA
; ORGANISM: Rattus rattus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(37)
; OTHER INFORMATION: Synthetic primer
US-09-591-306-33

Query Match          59.0%; Score 11.8; DB 7; Length 37;
Best Local Similarity 86.7%; Pred. No. 1.1e+04;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Qy 2 atgatgcttaaaagc 16
||| ||| |||||
Db 15 atggtgcgtataaagc 29

Search completed: October 2, 2001, 16:55:06
Job time: 17669 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 2, 2001, 16:18:46 ; Search time 876.95 seconds

(without alignments)
10.740 Million cell updates/sec

Title: US-09-757-100b-23

Perfect score: 15

Sequence: 1 gcgggctcacagtgg 15

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 730101 seqs, 313950809 residues

Total number of hits satisfying chosen parameters: 854978

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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14: /SIDS8/gcgdata/geneseq/geneseq/NA1993.DAT.*
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17: /SIDS8/gcgdata/geneseq/geneseq/NA1996.DAT.*
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21: /SIDS8/gcgdata/geneseq/geneseq/NA2000.DAT.*
22: /SIDS8/gcgdata/geneseq/geneseq/NA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15	100.0	15	22	Human focal adhesi
2	15	100.0	20	22	Human focal adhesi
c 3	13.4	89.3	31	22	Oligonucleotide si
c 4	11.8	78.7	20	19	Human NKCC2 gene e
5	11.8	78.7	24	20	PCR primer used to
6	11.8	78.7	31	18	Primer murF2. Syn
7	11.8	78.7	31	19	3' PCR primer used
8	11.8	78.7	31	20	PCR primer used to
9	11.8	78.7	39	11	Oligonucleotide ca
10	11.8	78.7	39	18	Primer murF4. Syn
11	11.8	78.7	39	20	PCR primer used to

12	11.8	78.7	44	21	AAA72106	HIV-1 gp41 C-helic
13	11.8	78.7	47	20	AAZ01125	probe for human PG
c 14	11.4	76.0	18	22	AAF94736	Rho G antisense ph
c 15	11.4	76.0	22	18	AA45334	Mycoplasma second
16	11.4	76.0	29	21	AAA04346	Polymorphic fragme
c 17	11.4	76.0	45	21	AAAD01093	PCR primer ZC17157
18	11.4	76.0	48	20	AAAX26801	Primer for 564/5/6
c 19	11.1	73.3	21	20	AAAX88971	Mouse vascular end
c 20	11	73.3	31	14	AAO40032	Sequence of forward
c 21	11	73.3	31	16	AAO89636	Forward primer 34F
c 22	10.8	72.0	15	22	AAF52005	IGF-I oligonucleot
c 23	10.8	72.0	15	22	AAF52006	IGF-I oligonucleot
c 24	10.8	72.0	17	18	AAFG2250	Granule bound star
25	10.8	72.0	18	20	AAZ30563	Human integrin alp
26	10.8	72.0	20	19	AAV18312	Measles virus L pr
27	10.8	72.0	20	20	AAZ22946	Primer specific fo
28	10.8	72.0	21	21	AAO65140	Primer #3 targeted
c 29	10.8	72.0	24	16	AAO03859	Primer BLGAMP4 for
30	10.8	72.0	24	17	AAAT31052	Human fibroblast g
c 31	10.8	72.0	24	18	AAAT79727	Beta-lactoglobulin
32	10.8	72.0	24	20	AAAX00053	Human FGFRI-P1 PCR
c 33	10.8	72.0	24	21	AAO65581	Murine proteinase
c 34	10.8	72.0	29	14	AAQ50767	ERM HIV target seq
c 35	10.8	72.0	29	16	AAO83139	HIVPCV12 No. 1960
c 36	10.8	72.0	30	13	AAO25250	NANBH PCR primer P
37	10.8	72.0	30	22	AAO2858	Human GPVI externa
38	10.8	72.0	32	14	AAO47793	Billirubin oxidase
c 39	10.8	72.0	32	22	AAQ92387	CD100 PCR primer S
40	10.8	72.0	36	21	AAZ57915	Escherichia coli t
41	10.8	72.0	40	21	AAZ55715	Anabaena variabill
42	10.8	72.0	50	21	AAZ47143	Liposome membrane
43	10.6	70.7	31	20	AAAX38989	Human genomic DNA
44	10.4	69.3	17	20	AAV92548	Human A-Raf substr
c 45	10.4	69.3	20	22	AAF92436	Human CYP3A relate

ALIGNMENTS

RESULT 1
AAC65555
ID AAC65555 standard; DNA; 15 BP.
XX
AC AAC65555;
XX
DT 12-FEB-2001 (first entry)
XX
DE Human focal adhesion kinase antisense sequence #21.
XX
KW Human; focal adhesion kinase; FAK; signal transduction; cancer;
KW embryonic development disorder; angiogenic disorder; wound healing;
KW antisense; phosphorothioate; ss.
XX
OS Homo sapiens.
XX
PN US6133031-A.
XX
PD 17-OCT-2000.
XX
PF 19-AUG-1999; 99US-0377310.
XX
PR 19-AUG-1999; 99US-0377310.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Monia BP, Gaarde WA;
XX
DR WPI; 2001-006141/01.
XX
PT New antisense compounds for inhibiting focal adhesion kinase
PT expression, especially useful for inhibiting retinal
PT neovascularization, or for diagnosing and treating e.g. colon cancer -
XX

PS Claim 3; Column 25; 30pp; English.

XX The present invention describes a number of phosphorothioate antisense
CC sequences to the human focal adhesion kinase (FAK) protein. This protein
CC is involved in integrin-mediated signal transduction, and is implicated
CC in cancer, particularly colon, breast and oral tumours, embryonic
CC development disorders, angiogenic disorders and wound healing. The
CC antisense sequences, including the one shown here, can be used in the
CC treatment of all of these.

XX Sequence 15 BP; 2 A; 4 C; 7 G; 2 T; 0 other;

Query Match 100.0%; Score 15; DB 22; Length 15;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gcgggctcacagtgg 15
Db 1 gcgggctcacagtgg 15
|||||

RESULT 2

AAC65535
ID AAC65535 standard; DNA; 20 BP.

XX AAC65535;

DT 12-FEB-2001 (first entry)

DE Human focal adhesion kinase antisense sequence #1.

XX Human; focal adhesion kinase; FAK; signal transduction; cancer;
KW embryonic development disorder; angiogenic disorder; wound healing;
KW antisense; phosphorothioate; ss.

XX Homo sapiens.

OS US613031-A.

PN 17-OCT-2000.

XX 19-AUG-1999; 99US-0377310.

XX 19-AUG-1999; 99US-0377310.

XX (ISIS-) ISIS PHARM INC.

XX Monia BP, Gaarde WA;

XX WPI; 2001-006141/01.

XX New antisense compounds for inhibiting focal adhesion kinase
PT expression, especially useful for inhibiting retinal
PT neovascularization, or for diagnosing and treating e.g. colon cancer -

PS Claim 3; Column 23; 30pp; English.

XX The present invention describes a number of phosphorothioate antisense
CC sequences to the human focal adhesion kinase (FAK) protein. This protein
CC is involved in integrin-mediated signal transduction, and is implicated
CC in cancer, particularly colon, breast and oral tumours, embryonic
CC development disorders, angiogenic disorders and wound healing. The
CC antisense sequences, including the one shown here, can be used in the
CC treatment of all of these.

XX Sequence 20 BP; 2 A; 7 C; 8 G; 3 T; 0 other;

Query Match 100.0%; Score 15; DB 22; Length 20;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gcgggctcacagtgg 15
Db 3 gcgggctcacagtgg 17
|||||

RESULT 3

AAC83406/c

ID AAC83406 standard; DNA; 31 BP.

XX AAC83406;

XX 26-FEB-2001 (first entry)

XX Oligonucleotide sfAZ2.

XX Translational reporter vector; renilla luciferase;

KW translational recoding; ss.

XX Synthetic.

XX US6143502-A.

XX 07-NOV-2000.

XX 31-MAR-1999; 99US-0282996.

XX 31-MAR-1999; 99US-0282996.

XX (UTAH) UNIV UTAH RES FOUND.

XX Grentzmann G, Atkins JF, Gesteland RF;

XX WPI; 2001-006431/01.

XX Translational reporter vector for quantification of translation
PT recoding in vivo and in vitro, comprises renilla luciferase gene,
PT polylinker for insertion of selected DNA and an out-of-frame firefly
PT luciferase gene -

XX Example 4; Column 33; 21pp; English.

XX The present invention relates to a translational reporter vector
CC selected from p2luc and p2luc1. The vectors have a polylinker
CC interposed between a renilla luciferase gene and a firefly luciferase
CC gene, which are out-of-frame with respect to each other but are
CC co-expressed upon recoding. The translational reporter vector is
CC useful for assaying translational recoding in vitro or in vivo.

XX Sequence 31 BP; 4 A; 10 C; 9 G; 8 T; 0 other;

Query Match 89.3%; Score 13.4; DB 22; Length 31;
Best Local Similarity 93.3%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 gcgggctcacagtgg 15
Db 23 GCGGGATCACAGTGG 9
|||||

RESULT 4

AAV45725/c

ID AAV45725 standard; DNA; 20 BP.

XX AAV45725;

XX 21-DEC-1998 (first entry)

XX Human NKCC2 gene exon 24 forward primer hNKCC2ex24.

XX Na-K-2Cl cotransporter; NKCC2; human; Bartter's syndrome;
KW transport; hypokalaemic alkalosis; hypercalciuria;
KW nephrocalcinosis; diagnosis; therapy; SSCP; primer; ss.

XX OS Synthetic.
 XX OS Homo sapiens.
 XX PN WO9829431-A1.
 XX PN 09-JUL-1998.
 XX PF 19-DEC-1997; 97WO-US233553.
 XX PR 31-DEC-1996; 96US-0778052.
 XX PA (UYVA) UNIV YALE.
 XX PI Lifton RP, Simon DB;
 XX DR WPI; 1998-388029/33.
 XX PT Thiazide sensitive cotransporter, ATP sensitive K channel and NaK2Cl cotransporter genes - useful for developing products for the diagnosis and treatment of ion transport disorders, e.g. Gitelman's Syndrome or Bartter's Syndrome
 XX PS Example 2; Page 65; 105pp; English.
 XX CC Primers hNKCC2ex24 forward and reverse (see AAV45725 and AAV45726, respectively) are designed to amplify exon 24 of the human NKCC2 gene (see AAV40562) that codes for Na-K-2Cl cotransporter NKCC2 protein (see AAV29683). Both primers are located within introns of the gene. 27 Sets of specific primers (see AAV45677-V45730) were used for SSCP analysis of NKCC2. Amplified products were analysed for molecular variants by electrophoresis, and identified variants were sequenced. Complete linkage of Bartter's syndrome with NKCC2 was demonstrated. Identification of the molecular basis of Bartter's syndrome allows for the genetic diagnosis of this disorder. The invention provides products and methods useful for diagnosis and treatment of Bartter's syndrome and other ion transport disorders.
 XX SQ Sequence 20 BP; 2 A; 7 C; 5 G; 6 T; 0 other;

Query Match 78.7%; Score 11.8; DB 19; Length 20;
 Best Local Similarity 86.7%; Pred. No. 1.2e+03;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 gcggggtcacagtgg 15
 ||| |||||
 Db 20 GAGGCTCACAGTGG 6

RESULT 5
 AAX36171
 ID AAX36171 standard; DNA; 24 BP.
 XX AC
 XX AAX36171;
 XX DT 15-JUL-1999 (first entry)
 XX DE PCR primer used to amplify a fragment of ICAM-6 nucleic acid.
 XX KW Intercellular adhesion molecule 6; ICAM-6; drug screening; therapy;
 XX KW Intercellular adhesion; inflammatory process; PCR primer; ss.
 XX OS Synthetic.
 XX PN WO9920762-A1.
 XX PD 29-APR-1999.
 XX PF 22-OCT-1998; 98WO-US22442.
 XX PR 22-OCT-1997; 97US-0955661.

XX PA (ICOS-) ICOS CORP.
 XX PI Loughney K, Staunton DE, Vazeau R;
 XX DR WPI; 1999-288308/24.
 XX PT New isolated intercellular adhesion molecule-6 used for, e.g. diagnosis of inflammatory processes
 XX PS Example 15; Page 53; 102pp; English.
 XX CC The specification describes an intercellular adhesion molecule (ICAM)-6 polypeptide. The ICAM-6 polypeptides and polynucleotides can be used for drug screening and developing products for therapy involving intercellular adhesion, e.g. in inflammatory processes. The products can also be used for detection, diagnosis and the production of transgenic animals. PCR primers AAX36170-73 were used in the course of the invention.
 XX SQ Sequence 24 BP; 6 A; 3 C; 10 G; 5 T; 0 other;

Query Match 78.7%; Score 11.8; DB 20; Length 24;
 Best Local Similarity 86.7%; Pred. No. 1.2e+03;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 gcggggtcacagtgg 15
 ||| |||||
 Db 10 gctggatcacagtgg 24

RESULT 6
 AAT63364
 ID AAT63364 standard; DNA; 31 BP.
 XX AC AAT63364;
 XX DT 07-SEP-1997 (first entry)
 XX DE Primer murF2.
 XX KW Recombinant plasmid; DNA immunisation; genetic vaccine; gene therapy; murF gene; Escherichia coli; primer; PCR;
 XX KW polymerase chain reaction; ss.
 XX OS Synthetic.
 XX PN WO9714805-A2.
 XX PD 24-APR-1997.
 XX PF 17-OCT-1996; 96WO-CA000693.
 XX PR 30-NOV-1995; 95US-0564973.
 XX PR 17-OCT-1995; 95US-0548059.
 XX PA (BIOS-) BIOSTAR INC.
 XX PI Morsey MA;
 XX DR WPI; 1997-245120/22.
 XX PT Culture system for stable high yield production of recombinant plasmids - using bacteria with modified chromosome that can survive only when plasmid is present and optionally foreign DNA expressible only in eukaryote(s)
 XX PS Example 1; Page 20; 46pp; English.
 XX CC Primers murF1 (AAT63363) and murF2 (AAT63364) were used to amplify the Escherichia coli murF gene (see also AAT63360) and were designed so as to allow in-frame fusion of the murF coding sequence to the

CC murE promoter. The murE promoter was subsequently amplified (see
 CC also AAF63365-66). An E. coli strain was constructed with an
 CC irreversible alteration (deletion) in its murF gene. This can
 CC be used for large-scale prodn. of recombinant plasmids.
 XX

SQ Sequence 31 BP; 6 A; 9 C; 13 G; 3 T; 0 other;

Query Match 78.7%; Score 11.8; DB 18; Length 31;
 Best Local Similarity 86.7%; Pred. No. 1.2e+03;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gcgggctcacagtgg 15
 || |||| |||||
 Db 12 gcaggctgacagtgg 26

RESULT 7
 AAV42721
 ID AAV42721 standard; DNA; 31 BP.
 AC AAV42721;
 XX
 XX 14-OCT-1998 (first entry)
 DT
 DE 3' PCR primer used to amplify human furin cDNA.
 XX
 XX Retroviral vector; gene delivery vehicle; expression; PCR primer;
 KW non-immunogenic selectable marker; gene therapy; activation;
 KW human; furin; ablation therapy; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 XX WO9830709-A2.
 PN
 XX 16-JUL-1998.
 PD
 XX 14-JAN-1998; 98WO-US00715.
 PF
 XX 13-JAN-1998; 98US-0038339.
 PR
 PR 14-JAN-1997; 97US-0038473.
 PR 27-FEB-1997; 97US-0038339.
 XX

(CHAD/) CHADA S.
 PA (JOLLY) JOLLY D J.
 PA (MOOR/) MOORE M D.
 XX
 PI Chada S, Jolly DJ, Moore MD;
 DR WPI; 1998-399153/34.
 XX
 XX Non-immunogenic pro-drug activating enzyme(s) and selectable
 PT marker(s) - are used in gene therapy for the treatment of a wide
 PT variety of disorder(s)
 XX

PS Example 8; Page 53; 121pp; English.

CC PCR primers AAV42720-21 were used to amplify human furin cDNA (see
 CC AAV42731). The amplified product is used in the retroviral vector of the
 CC invention to encode a cell bound prodrug convertase for ablation therapy.
 CC The specification describes a gene delivery vehicle which directs
 CC expression of a non-immunogenic selectable marker or molecule which is
 CC capable of activating a previously inactive compound. Vectors expressing
 CC the markers and a heterologous sequence are useful in gene therapy. The
 CC vectors can be used to deliver a molecule into a target area where it may
 CC cause the activation of a previously inactive substance.
 XX

SQ Sequence 31 BP; 5 A; 12 C; 10 G; 4 T; 0 other;

Query Match 78.7%; Score 11.8; DB 19; Length 31;
 Best Local Similarity 86.7%; Pred. No. 1.2e+03;

Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 gcgggctcacagtgg 15
 || |||| |||||
 Db 13 gtgggctcacagagg 27

RESULT 8

AAx86099
 ID AAX86099 standard; DNA; 31 BP.
 XX

AC AAX86099;
 XX
 XX 13-SEP-1999 (first entry)
 DT
 DE PCR primer used to amplify the murF gene.
 XX

KW Culture system; high level production; recombinant plasmid; murF;
 KW plasmid replication; plasmid production; DNA immunisation; gene therapy;
 KW PCR primer; ss.
 XX
 OS Synthetic.
 XX
 XX US5922583-A.
 PN
 XX 13-JUL-1999.
 PD
 XX 16-OCT-1996; 96US-0732612.
 PF
 XX 16-OCT-1996; 96US-0732612.
 PR
 PR 17-OCT-1995; 95US-0548059.
 PR 30-NOV-1995; 95US-0564973.
 XX

PA (BIOS-) BIOSTAR INC.
 XX
 XX Morsey MA;
 PI
 XX WPI; 1999-404463/34.
 XX

PT Culture system for stable and high-level production of DNA contained
 PT on recombinant plasmids, with improved plasmid stability
 XX
 PS Example 1; Column 13; 27pp; English.

CC The specification describes a culture system for stable high-level
 CC production of recombinant plasmids. The method comprises propagating
 CC irreversibly altered bacterial cells under conditions such that cell
 CC viability is dependent on the recombinant plasmid. The system is used
 CC is for the replication and high-level production of structurally and
 CC genetically stable recombinant plasmids carrying DNA, this DNA can
 CC then be used in DNA immunisation or gene therapy. PCR primers
 CC AAX86098-99 were used to amplify the murF gene, for use in the method
 CC of the invention.
 XX

SQ Sequence 31 BP; 6 A; 9 C; 13 G; 3 T; 0 other;

Query Match 78.7%; Score 11.8; DB 20; Length 31;
 Best Local Similarity 86.7%; Pred. No. 1.2e+03;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gcgggctcacagtgg 15
 || |||| |||||
 Db 12 gcaggctgacagtgg 26

RESULT 9

AAQ04938
 ID AAQ04938 standard; DNA; 39 BP.
 XX
 AC AAQ04938;
 XX

DT 24-OCT-1990 (first entry)

```

XX DE Oligonucleotide carrying mutation for factor VIII gene.
XX KW Human factor VIII analogue; ss.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT mutation 18..23
XX FT /*tag= a
XX PN WO9005530-A.
XX PD 31-MAY-1990.
XX PF 14-NOV-1989; 89WO-0005049.
XX PR 14-NOV-1988; 88US-0270882.
XX PA (GENE-) GENETICS INST INC.
XX PI Kaufman RJ, Pittman DD;
XX DR WPI; 1990-193265/25.
XX DE New hybrid DNA encoding hybrid procoagulant proteins -
XX FT prepd. by modifying DNA encoding human factor VIII.
XX PS Disclosure; ; pp; English.
XX CC Factor VIII analogue is sufficiently mutated from the original gene
XX CC that it is not recognised by blood Abs of the patient. The analogue
XX CC is composed of human FVIII but carries the B-domain of human FV in
XX CC place of the FVIII B-domain.
XX CC Oligonucleotides can be used to alter the profile of the blood
XX CC factor without significantly altering its activity.
XX SQ Sequence 39 BP; 9 A; 11 C; 11 G; 8 T; 0 other;

Query Match 78.7%; Score 11.8; DB 11; Length 39;
Best Local Similarity 86.7%; Pred. No. 1.3e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 gcgggctcacagtgg 15
Db 20 gcgtgctcacagtgg 34
||| ||||| |||||

RESULT 10
AAT63369
ID AAT63369 standard; DNA; 39 BP.
XX AC AAT63369;
XX DT 07-SEP-1997 (first entry)
XX DE Primer murF4.
XX KW Recombinant plasmid; DNA immunisation; genetic vaccine;
XX KW gene therapy; murF gene; Escherichia coli; primer; PCR;
XX KW polymerase chain reaction; ss.
XX OS Synthetic.
XX PN WO9714805-A2.
XX PD 24-APR-1997.
XX PF 17-OCT-1996; 96WO-CA00693.
XX PR 30-NOV-1995; 95US-0564973.
XX PR 17-OCT-1995; 95US-0548059.

```

```

XX PA (BIOS-) BIOSTAR INC.
XX PI Morsey MA;
XX DR WPI; 1997-245120/22.
XX DE Culture system for stable high yield production of recombinant
XX FT plasmids - using bacteria with modified chromosome that can survive
XX FT only when plasmid is present and optionally foreign DNA expressible
XX FT only in eukaryote(s)
XX PS Example 2; Page 23; 46pp; English.
XX CC Primers murF3 (AAT63368) and murF4 (AAT63369) were used to amplify the
XX CC temperature-sensitive murF gene (see also AAT63360) from Escherichia
XX CC coli TKL-68. The amplified nucleotide sequence was cloned into
XX CC the BamHI site of pUC19, and can be used to produce temperature-
XX CC sensitive bacterial host cells useful for large-scale prodn. of
XX CC recombinant plasmids.
XX SQ Sequence 39 BP; 9 A; 10 C; 15 G; 5 T; 0 other;

Query Match 78.7%; Score 11.8; DB 18; Length 39;
Best Local Similarity 86.7%; Pred. No. 1.3e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 gcgggctcacagtgg 15
Db 20 gcaggctgacagtgg 34
|| |||| |||||

RESULT 11
AAX86104
ID AAX86104 standard; DNA; 39 BP.
XX AC AAX86104;
XX DT 13-SEP-1999 (first entry)
XX DE PCR primer used to amplify the murF gene.
XX KW Culture system; high level production; recombinant plasmid; murF;
XX KW plasmid replication; plasmid production; DNA immunisation; gene therapy;
XX KW PCR primer; ss.
XX OS Synthetic.
XX PN US5922583-A.
XX PD 13-JUL-1999.
XX PF 16-OCT-1996; 96US-0732612.
XX PR 16-OCT-1996; 96US-0732612.
XX PR 17-OCT-1995; 95US-0548059.
XX PR 30-NOV-1995; 95US-0564973.
XX PA (BIOS-) BIOSTAR INC.
XX PI Morsey MA;
XX DR WPI; 1999-404463/34.
XX DE Culture system for stable and high-level production of DNA contained
XX FT on recombinant plasmids, with improved plasmid stability
XX PS Example 2; Column 15; 27pp; English.
XX CC The specification describes a culture system for stable high-level
XX CC production of recombinant plasmids. The method comprises propagating
XX CC irreversibly altered bacterial cells under conditions such that cell

```

CC viability is dependent on the recombinant plasmid. The system is used
 CC is for the replication and high-level production of structurally and
 CC genetically stable recombinant plasmids carrying DNA, this DNA can
 CC then be used in DNA immunisation or gene therapy, PCR primers
 CC AAX86102-03 were used to amplify the murf gene, for use in the method
 CC of the invention.

XX Sequence 39 BP; 9 A; 10 C; 15 G; 5 T; 0 other;
 SQ

Query Match 78.7%; Score 11.8; DB 20; Length 39;
 Best Local Similarity 86.7%; Pred. No. 1.3e+03;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gcggggtcacagtgg 15
 || |||| |||||
 Db 20 gcaggctgacagtgg 34

RESULT 12

AAA72106
 ID AAA72106 standard; DNA; 44 BP.

XX AC AAA72106;

XX DT 24-NOV-2000 (first entry)

XX DE HIV-1 gp41 C-helical domain 5' PCR primer.

XX KW HIV-1; gp41; N-helical domain; heptad repeat region; C-helical domain;
 KW gp41 transmembrane-proximal amphipathic alpha-helical segment;
 KW core 6-helix bundle; viral entry inhibition; immunogenic;
 KW antibody; humoral response; broad spectrum vaccine; anti-HIV;
 KW envelope glycoprotein; prophylaxis; therapy; PCR primer; ss.

XX OS Human Immunodeficiency virus type 1.

XX PN WO200040616-A1.

XX PD 13-JUL-2000.

XX PF 10-JAN-2000; 2000WO-US00456.

XX PR 08-JAN-1999; 99US-0115404.

XX PR 07-JAN-2000; 2000US-0480336.

XX PA (WILD/) WILD C T.

XX PA (WEIS/) WEISS C D.

XX PI WILD CT, Weiss CD;

XX DR WPI; 2000-465959/40.

XX PT Raising neutralizing antibody response to human immunodeficiency virus,
 PT comprises administering a polypeptide capable of forming a stable
 PT coiled-coil solution structure.

XX PS Example 5; Page 54; 97pp; English.

XX CC The invention relates to raising a neutralising antibody response to a
 CC broad spectrum of HIV (human immunodeficiency virus) strains and
 CC isolates, comprising the administration of a peptide which corresponds
 CC to or mimics highly conserved portions of the gp41 envelope glycoprotein
 CC which are important in mediating the process of viral entry into host
 CC cells. Such peptides can correspond to or mimic the coiled coil
 CC solution structure of the N-helical domain (the heptad repeat
 CC region), or can correspond to mimic the C-helical domain (the
 CC transmembrane-proximal amphipathic alpha-helical segment), or the
 CC gp41 core 6-helix bundle, which is formed by the interaction of
 CC the N- and C-helical domains of three gp41 proteins. The peptides
 CC can be administered either singly or as a combination (particularly
 CC a combination of N-helical and C-helical peptides), and can be
 CC multimerised. For example, N- and C-helical domain peptides can be

CC alternately linked together to form a peptide which mimics the core
 CC 6-helix bundle. Administration of the peptide(s) generates a humoral
 CC response, with the production of antibodies against gp41 structures
 CC involved in viral entry. As these portions of gp41 are well conserved,
 CC such antibodies may be effective against a broad range of HIV strains
 CC and isolates. The peptide compositions may be administered as a
 CC prophylactic or therapeutic vaccine to generate antibodies which reduce
 CC or inhibit the ability of HIV to infect uninfected cells. A composition
 CC comprising polyclonal or monoclonal antibodies can be administered to
 CC reduce HIV infection of uninfected cells. Antibodies raised against
 CC entry-relevant gp41 structures may also be used therapeutically and as
 CC tools to further elucidate the mechanism of HIV cell entry.
 CC Sequences AAA72104-A72107 represent PCR primers used in an
 CC exemplification of the invention to construct DNA (AAA72102) encoding a
 CC protein construct (AAB14603) comprising the N- and C-helical domains of
 CC HIV-1 gp41 separated by a short peptide linker.

XX SQ Sequence 44 BP; 13 A; 10 C; 15 G; 6 T; 0 other;

Query Match 78.7%; Score 11.8; DB 21; Length 44;
 Best Local Similarity 86.7%; Pred. No. 1.3e+03;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gcggggtcacagtgg 15
 || |||| |||||
 Db 9 gcggggtcacagtgg 23

RESULT 13

AAZ01125

ID AAZ01125 standard; DNA; 47 BP.

XX AC AAZ01125;

XX DT 27-SEP-1999 (first entry)

XX DE Probe for human PGI biallelic marker 4-50-293.

XX KW PGI gene; biallelic marker; PCR primer; PGI-related biallelic marker;
 KW cancer; prostate cancer; diagnosis; therapy; prostate specific antigen;
 KW PSA; human; ss.

XX OS Synthetic.

XX OS Homo sapiens.

XX PN WO9932644-A2.

XX PD 01-JUL-1999.

XX PF 22-DEC-1998; 98WO-IB02133.

XX PR 09-SEP-1998; 98US-0099658.

XX PR 22-DEC-1997; 97US-0996306.

XX PA (GEST) GENSET.

XX PI Blumenfeld M, Bougueleret L, Chumakov I, Cohen D;

XX DR WPI; 1999-405178/34.

XX PT Use of a prostate cancer associated gene and biallelic markers
 PT derived from it

XX PS Claim 4; Page 328; 385pp; English.

XX CC The invention relates to a mammalian PGI gene and protein, and a set of
 CC PGI biallelic markers. The PGI polynucleotide and biallelic markers are
 CC used in a hybridisation assay, a sequencing assay, or in an
 CC allele-specific amplification assay for determining the identity of a
 CC nucleotide at a PGI-related biallelic marker. The methods can be used to
 CC detect and to assess the risk of developing cancer or prostate cancer.
 CC Early-stage diagnosis of prostate cancer relies on prostate specific

CC antigen (PSA) dosage. However, the effectiveness of this is limited due
 CC to its inability to discriminate between malignant and non-malignant
 CC affections of the organ. A need exists for both a reliable diagnostic
 CC procedure which would enable early-stage diagnosis, and for preventative
 CC and curative treatments of the disease. The PGI gene can be used for
 CC detection of prostate cancer, and the risk of developing it in the
 CC future, and can also be used to determine therapies for the disease.
 XX
 SQ Sequence 47 BP; 14 A; 9 C; 14 G; 10 T; 0 other;

Query Match 78.7%; Score 11.8; DB 20; Length 47;
 Best Local Similarity 86.7%; Pred. No. 1.3e+03;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gcgggctcacagtgg 15
 | | | | | | | | | | | | | | |
 Db 12 gggggctgacagtgg 26

RESULT 14
 AAF94736/c
 ID AAF94736 standard; DNA; 18 BP.

XX AAF94736;

AC AAF94736;

XX 23-MAY-2001 (first entry)

XX Rho G antisense phosphorothioate oligonucleotide SEQ ID 160.

XX Rho; GTP binding protein; phosphorothioate antisense oligonucleotide;
 KW RhoA; RhoB; RhoC; RhoG; Rac 1; cdc42; hyperproliferative condition;
 KW cancer; wound healing; clotting; ischaemia; reperfusion; reoxygenation;
 KW ss.

XX Homo sapiens.

XX WO200115739-A1.

XX 08-MAR-2001.

XX 18-AUG-2000; 2000WO-US22808.

XX 31-AUG-1999; 99US-0387341.

XX (ISIS-) ISIS PHARM INC.

XX Roberts ML, Cowsert LM;

XX WPI; 2001-191677/19.

XX An antisense compound targeted to a nucleic acid molecule encoding a
 PT member of the human Rho family of small GTP binding proteins useful for
 PT treating e.g. cancer and ischaemia -

XX Example 18; Page 81; 156pp; English.

XX This invention relates to an antisense compound targeted to a nucleic
 CC acid molecule encoding a member of the human Rho family of small GTP
 CC binding proteins, where the antisense compound inhibits the expression of
 CC the member of the human Rho family. The invention includes antisense
 CC oligonucleotides AAF94580 - AAF94637 which target a RhoA nucleotide
 CC sequence, AAF94645 - AAF94684 which target a RhoB nucleotide sequence,
 CC AAF94686 - AAF94725 which target a RhoC nucleotide sequence, AAF94727 -
 CC AAF94766 which target RhoG nucleotide sequence, AAF94769 - AAF94790 which
 CC target a Rac 1 nucleotide sequence and AAF94795 - AAF94809 which target
 CC cdc42 nucleotide sequence. The antisense compound is useful for treating
 CC hyperproliferative conditions, especially cancer, abnormal wound healing
 CC or clotting conditions and ischaemia/reperfusion or reoxygenation injury.
 CC The compound may also be used to diagnose the above conditions.

XX Sequence 18 BP; 1 A; 6 C; 6 G; 5 T; 0 other;

Query Match 76.0%; Score 11.4; DB 22; Length 18;
 Best Local Similarity 92.3%; Pred. No. 2e+03;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 cgggctcacagtgg 14
 | | | | | | | | | | | | | | |
 Db 17 CGGGCGCACAGTG 5

RESULT 15
 AAT45334/c
 ID AAT45334 standard; DNA; 22 BP.

XX AAT45334;

XX 10-JUL-1997 (first entry)

XX Mycoplasma second stage PCR primer M34.

XX Polymerase chain reaction; Mycoplasma; M.fermentans; M.hyorhinis;
 KW M.arginini; M.pirum; M.hominis; M.salivarium; M. orale; detection; ss.

XX Synthetic.

XX WO9636735-A1.

XX 21-NOV-1996.

XX 13-MAY-1996; 96WO-US07116.

XX 19-MAY-1995; 95US-0445289.

XX (AMTY-) AMERICAN TYPE CULTURE COLLECTION.

XX Roblin RO;

XX WPI; 1997-020833/02.

XX Two-stage PCR system using sets of mixed and single sequence primers
 PT - useful for sensitive detection of mycobacteria and
 PT mycobacteria-like organism contamination of nucleic acid samples

XX Claim 18; Page 30; 42pp; English.

XX The present sequence is the M34 primer involved in the second stage of
 CC PCR in the novel method for amplifying a target segment of nucleic acid
 CC in a sample nucleic acid mixture. It is part of the second stage primer
 CC mixture that is made up of 3 different primers:- F2, R2, and M34 in
 CC relative molar ratios of 0.25: 0.125: 1. Using both first and second
 CC stage primers in the nested PCR method provides an enhanced system for
 CC specific, sensitive and rapid detection of the presence and
 CC identification of Mycoplasma species and Mycoplasma-like organism (MLO)
 CC contaminants contained in a sample of nucleic acid. The method allows
 CC detection of less than 200 colony forming units (cfu)/ml of Mycoplasma
 CC species M.fermentans, M.hyorhinis, M.arginini, M.pirum, M.hominis and
 CC M.salivarium and 350 cfu/ml for M. orale. This compares to detection
 CC levels of 1000 cfu/ml for known Mycoplasma detection systems. Also,
 CC unlike prior art Mycoplasma detection systems, the new method and
 CC primers can detect the MLO contaminant Acholeplasma laidlawii at
 CC levels as low as 20 cfu/ml.

XX Sequence 22 BP; 1 A; 8 C; 4 G; 9 T; 0 other;

Query Match 76.0%; Score 11.4; DB 18; Length 22;
 Best Local Similarity 92.3%; Pred. No. 2e+03;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 gggctcacagtgg 15
 | | | | | | | | | | | | | | |
 Db 13 GGGCACACAGTGG 1

Search completed: October 2, 2001, 16:18:47
Job time: 15491 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: October 2, 2001, 16:03:53 ; Search time 417.38 Seconds
(without alignments)
9.071 Million cell updates/sec

Title: US-09-757-100B-20

Perfect score: 20

Sequence: 1 catgatgcttaaaagcttac 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 324599 seqs, 9465562 residues

Total number of hits satisfying chosen parameters: 460742

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_NA:*

1: /cgn2_6/ptodata/1/ina/5A_COMB.seq.*

2: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*

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4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*

5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq.*

6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	3	US-09-377-310-20
2	15	75.0	15	3	US-09-377-310-40
c 3	13.8	69.0	29	1	US-08-244-492A-7
c 4	13.8	69.0	29	1	US-08-709-915-9
5	13.4	67.0	44	2	US-08-818-604-5
c 6	13.2	66.0	33	1	US-08-285-936-14
c 7	13.2	66.0	33	1	US-08-487-860-14
c 8	13.2	66.0	33	2	US-08-762-308-5
c 9	13.2	66.0	33	5	PCT-US95-04221-5
c 10	12.6	63.0	36	3	US-08-961-083-418
c 11	12.4	62.0	20	4	US-09-488-671-75
c 12	12.2	61.0	25	1	US-08-348-891A-10
c 13	12.2	61.0	25	1	US-08-505-817-10
c 14	12.2	61.0	27	3	US-08-985-162-1042
c 15	12.2	61.0	27	3	US-08-964-268-13
c 16	12.2	61.0	29	2	US-08-871-266B-4
c 17	12.2	61.0	29	2	US-08-819-458A-6
c 18	12.2	61.0	29	2	US-09-018-864A-4
c 19	12.2	61.0	29	3	US-08-871-267B-6
c 20	12.2	61.0	29	4	US-08-821-994-24
c 21	12.2	61.0	30	1	US-08-583-318-2
c 22	12.2	61.0	33	3	US-08-868-594-5
c 23	12.2	61.0	33	3	US-08-961-083-330
c 24	12.2	61.0	33	4	US-09-305-408-3
c 25	12	60.0	31	3	US-08-961-083-272
c 26	12	60.0	34	3	US-08-961-083-316
27	12	60.0	42	6	5256642-28

28	12	60.0	42	6	5472939-28	Patent No. 5472939
29	12	60.0	44	2	US-08-327-451E-29	Sequence 29, Appl
30	12	60.0	44	2	US-08-458-109-29	Sequence 29, Appl
c 31	11.8	59.0	21	5	US-08-487-867-31	Sequence 31, Appl
c 32	11.8	59.0	21	5	PCT-US96-09358-31	Sequence 31, Appl
33	11.8	59.0	27	3	US-08-985-162-1497	Sequence 1497, Ap
34	11.8	59.0	30	1	US-07-832-905B-84	Sequence 84, Appl
35	11.8	59.0	30	2	US-08-700-757-84	Sequence 84, Appl
c 36	11.8	59.0	34	2	US-08-521-871A-7	Sequence 7, Appli
37	11.8	59.0	37	2	US-08-202-044-28	Sequence 28, Appl
38	11.8	59.0	37	4	US-08-751-344B-27	Sequence 27, Appl
c 39	11.8	59.0	45	2	US-08-244-434-8	Sequence 8, Appli
c 40	11.6	58.0	21	4	US-09-581-493-6	Sequence 6, Appli
c 41	11.6	58.0	23	2	US-09-100-398-1	Sequence 1, Appli
c 42	11.6	58.0	25	2	US-08-828-010-8	Sequence 8, Appli
43	11.6	58.0	26	2	US-08-373-284A-3	Sequence 3, Appli
44	11.6	58.0	26	2	US-08-514-542C-9	Sequence 9, Appli
45	11.6	58.0	27	3	US-08-985-162-1512	Sequence 1512, Ap

ALIGNMENTS

RESULT 1

US-09-377-310-20

; Sequence 20, Application US/09377310B

; Patent No. 6133031

; GENERAL INFORMATION:

; APPLICANT: Monia, Brett P.

; APPLICANT: Gaarde, William A.

; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase

; TITLE OF INVENTION: Expression

; FILE REFERENCE: ISPH-0389

; CURRENT APPLICATION NUMBER: US/09/377,310B

; CURRENT FILING DATE: 1999-08-19

; NUMBER OF SEQ ID NOS: 43

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 20

; LENGTH: 20

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: antisense sequence

US-09-377-310-20

Query Match 100.0%; Score 20; DB 3; Length 20;

Best Local Similarity 100.0%; Pred. NO. 0.22;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 catgatgcttaaaagcttac 20

|||||

Db 1 catgatgcttaaaagcttac 20

RESULT 2

US-09-377-310-40

; Sequence 40, Application US/09377310B

; Patent No. 6133031

; GENERAL INFORMATION:

; APPLICANT: Monia, Brett P.

; APPLICANT: Gaarde, William A.

; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase

; TITLE OF INVENTION: Expression

; FILE REFERENCE: ISPH-0389

; CURRENT APPLICATION NUMBER: US/09/377,310B

; CURRENT FILING DATE: 1999-08-19

; NUMBER OF SEQ ID NOS: 43

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 40

; LENGTH: 15

; TYPE: DNA

; ORGANISM: Artificial Sequence


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RESULT 5
US-08-818-604-5
; Sequence 5, Application US/08818604C
; Patent No. 5958713
; GENERAL INFORMATION:
; APPLICANT: Thastrup, Ole
; APPLICANT: Tullin, Soren
; APPLICANT: Poulsen, Lars
; APPLICANT: Bjorn, Sara
; TITLE OF INVENTION: A Method of Detecting Biologically
; FILE REFERENCE: 4301.204-US
; CURRENT APPLICATION NUMBER: US/08/818,604C
; CURRENT FILING DATE: 1997-03-14
; EARLIER APPLICATION NUMBER: 0110/95
; EARLIER FILING DATE: 1995-01-31
; EARLIER APPLICATION NUMBER: 0982/95
; EARLIER FILING DATE: 1995-09-07
; EARLIER APPLICATION NUMBER: PCT/DK96/00052
; EARLIER FILING DATE: 1996-01-31
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 44
; TYPE: DNA
; ORGANISM: Aequorea victoria
US-08-818-604-5

Query Match 67.0%; Score 13.4; DB 2; Length 44;
Best Local Similarity 93.3%; Pred. No. 3.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 atgcttaaaagctta 19
|| |||||
Db 5 attcttaaaagctta 19

RESULT 6
US-08-285-936-14/c
; Sequence 14, Application US/08285936
; Patent No. 5728821
; GENERAL INFORMATION:
; APPLICANT: Yelton, Dale
; APPLICANT: Glaser, Scott
; APPLICANT: Huse, William
; APPLICANT: Rosok, Mae J.
; TITLE OF INVENTION: No. 5728821el Mutant BR96 Antibodies and
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 11150 Santa Monica Blvd., Suite 400
; CITY: Los Angeles
; STATE: CA
; COUNTRY: USA
; ZIP: 90025-3395
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/285,936
; FILING DATE: 04-AUG-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Adriano, Sarah B.
; REGISTRATION NUMBER: 34,470
; REFERENCE/DOCKET NUMBER: 30436.16US01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 310-445-9031
; TELEFAX: 310-445-9031
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-285-936-14

Query Match 67.0%; Score 13.4; DB 2; Length 44;
Best Local Similarity 93.3%; Pred. No. 3.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 atgcttaaaagctta 19
|| |||||
Db 5 attcttaaaagctta 19
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TELEPHONE: 310-445-1140
TELEFAX: 310-445-9031
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-285-936-14

Query Match 66.0%; Score 13.2; DB 1; Length 33;
Best Local Similarity 83.3%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 tgatgcttaaaagcttac 20
| |||| |||||
Db 28 TTATGCCTAAAGCTTTC 11

RESULT 7
US-08-487-860-14/c
; Sequence 14, Application US/08487860
; Patent No. 5792456
; GENERAL INFORMATION:
; APPLICANT: Yelton, Dale
; APPLICANT: Glaser, Scott
; APPLICANT: Huse, William
; APPLICANT: Rosok, Mae J.
; TITLE OF INVENTION: No. 5792456el Mutant BR96 Antibodies and
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 11150 Santa Monica Blvd., Suite 400
; CITY: Los Angeles
; STATE: CA
; COUNTRY: USA
; ZIP: 90025-3395
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,860
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Adriano, Sarah B.
; REGISTRATION NUMBER: 34,470
; REFERENCE/DOCKET NUMBER: 30436.16US01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 310-445-1140
; TELEFAX: 310-445-9031
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-487-860-14

Query Match 66.0%; Score 13.2; DB 1; Length 33;
Best Local Similarity 83.3%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 tgatgcttaaaagcttac 20
| |||| |||||
Db 28 TTATGCCTAAAGCTTTC 11
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RESULT 8
US-08-762-308-5/c
; Sequence 5, Application US/08762308
; Patent No. 5925548
; GENERAL INFORMATION:
; APPLICANT: Beutler, Bruce A.
; APPLICANT: Bazzoni, Flavia M.
; TITLE OF INVENTION: MODIFIED RECEPTORS THAT CONTINUOUSLY
; TITLE OF INVENTION: SIGNAL
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/762.308
; FILING DATE: 09-DEC-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/224.593
; FILING DATE: 05-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: UFSO-335--1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 418-3000
; TELEFAX: 474-7577
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-762-308-5

Query Match 66.0%; Score 13.2; DB 2; Length 33;
Best Local Similarity 83.3%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 2 atgatgcttaaaagctta 19
| ||||| |||||
Db 23 AGGATGCTTGGAGCTTA 6

RESULT 9
PCT-US95-04221-5/c
; Sequence 5, Application PC/TUS9504221
; GENERAL INFORMATION:
; APPLICANT: BOARD OF REGENTS, THE UNIVERSITY OF TEXAS
; APPLICANT: NAME:
; APPLICANT: SYSTEM
; APPLICANT: STREET: 201 West 7th Street
; APPLICANT: CITY: Austin
; APPLICANT: STATE: Texas
; APPLICANT: COUNTRY: United States of America
; APPLICANT: POSTAL CODE: 78701
; APPLICANT: TELEPHONE NO: (512) 499-4462
; APPLICANT: TELEFAX: (512) 499-4523
; TITLE OF INVENTION: MODIFIED RECEPTORS THAT
; TITLE OF INVENTION: CONTINUOUSLY SIGNAL

; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04221
; FILING DATE: CONCURRENTLY HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US SN 08/224.593
; FILING DATE: 05 APRIL 1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: KITCHELL, BARBARA S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: UFTD335P--
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (713) 789-2679
; TELEX: 79-0924
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
PCT-US95-04221-5

Query Match 66.0%; Score 13.2; DB 5; Length 33;
Best Local Similarity 83.3%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 2 atgatgcttaaaagctta 19
| ||||| |||||
Db 23 AGGATGCTTGGAGCTTA 6

RESULT 10
US-08-961-083-418/c
; Sequence 418, Application US/08961083
; Patent No. 6159469
; GENERAL INFORMATION:
; APPLICANT: Choi et. al.
; TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
; NUMBER OF SEQUENCES: 452
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961.083
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:

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; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB340P2
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 418:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; US-08-961-083-418

Query Match          63.0%; Score 12.6; DB 3; Length 36;
Best Local Similarity 78.9%; Pred. No. 8.1e+02;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 atgatgcttaaaagcttac 20
   || ||| | | |||||
Db 21 ATTAATGTTGATAAGCTTAC 3

RESULT 11
; US-09-488-671-75
; Sequence 75, Application US/09488671A
; Patent No. 6187545
; GENERAL INFORMATION:
; APPLICANT: Robert McKay
; APPLICANT: Madeline M. Butler
; APPLICANT: Jacqueline Wyatt
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF PEPCK-CYTOSOLIC EXPRESSION
; FILE REFERENCE: RTS-0123
; CURRENT APPLICATION NUMBER: US/09/488,671A
; CURRENT FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 177
; SEQ ID NO 75
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
; US-09-488-671-75

Query Match          62.0%; Score 12.4; DB 4; Length 20;
Best Local Similarity 92.9%; Pred. No. 9.7e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 gatgcttaaaagct 17
   ||||| |||||
Db 1 gatgctgaaaagct 14

RESULT 12
; US-08-348-891A-10/c
; Sequence 10, Application US/08348891A
; Patent No. 5654136
; GENERAL INFORMATION:
; APPLICANT: SASAKI, Keiko
; APPLICANT: MORI, Takayuki
; APPLICANT: MAKINO, Satoshi
; TITLE OF INVENTION: ATTENUATED MEASLES VIRUS VACCINE,
; CONTAINING SPECIFIC NUCLEOTIDE SEQUENCE AND A METHOD FOR
; ITS ABSOLUTE IDENTIFICATION
; TITLE OF INVENTION: ITS ABSOLUTE IDENTIFICATION
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: YOUNG & THOMPSON
; STREET: 745 South 23rd Street
; CITY: Arlington
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/905,817
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; STREET: 745 South 23rd Street
; CITY: Arlington
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/348,891A
; FILING DATE: 25-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/848,400
; FILING DATE: 10-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 3-293625
; FILING DATE: 14-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: PATCH, Andrew J.
; REGISTRATION NUMBER: 32,925
; REFERENCE/DOCKET NUMBER: KP-7501
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-521-2297
; TELEFAX: 703-685-0573
; TELEX: 248425 EMBON
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-348-891A-10

Query Match          61.0%; Score 12.2; DB 1; Length 25;
Best Local Similarity 82.4%; Pred. No. 1.2e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 catgatgcttaaaagct 17
   ||||| ||| | |
Db 25 CATGATGCTTGAGAGGT 9

RESULT 13
; US-08-905-817-10/c
; Sequence 10, Application US/08905817
; Patent No. 5824777
; GENERAL INFORMATION:
; APPLICANT: SASAKI, Keiko
; APPLICANT: MORI, Takayuki
; APPLICANT: MAKINO, Satoshi
; TITLE OF INVENTION: ATTENUATED MEASLES VIRUS VACCINE,
; CONTAINING SPECIFIC NUCLEOTIDE SEQUENCE AND A METHOD FOR
; ITS ABSOLUTE IDENTIFICATION
; TITLE OF INVENTION: ITS ABSOLUTE IDENTIFICATION
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: YOUNG & THOMPSON
; STREET: 745 South 23rd Street
; CITY: Arlington
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/905,817
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;; FILING DATE: 04-AUG-1997;
;; CLASSIFICATION: 435
;; PRIOR APPLICATION NUMBER: US 08/348,891
;; FILING DATE: 25-NOV-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/848,400
;; FILING DATE: 10-MAR-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: JP 3-293625
;; FILING DATE: 14-OCT-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: PATCH, Andrew J.
;; REGISTRATION NUMBER: 32,925
;; REFERENCE/DOCKET NUMBER: KP-7501A
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 703-521-2297
;; TELEFAX: 703-685-0573
;; TELEX: 248425 EMBON
;; INFORMATION FOR SEQ ID NO: 10:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 25 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: cDNA
US-08-905-817-10

Query Match 61.0%; Score 12.2; DB 1; Length 25;
Best Local Similarity 82.4%; Pred. No. 1.2e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 catgatgtcttaaaagct 17
||||||| | | |
Db 25 CATGATGCTTGAGAGT 9

RESULT 14
US-08-985-162-1042
; Sequence 1042, Application US/08985162
; Patent No. 6057156
; GENERAL INFORMATION:
; APPLICANT: Akhtar, Saghir
; APPLICANT: Fell, Patricia
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT
; TITLE OF INVENTION: OF DISEASES OR CONDITIONS RELATED
; TITLE OF INVENTION: TO LEVELS OF EPIDERMAL GROWTH
; NUMBER OF SEQUENCES: 1877
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Fastseq for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,162
; FILING DATE: 04 December 1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/036,476
; FILING DATE: 31 January 1997
; ATTORNEY/AGENT INFORMATION:

;; NAME: Warburg, Richard J.
;; REGISTRATION NUMBER: 32,327
;; REFERENCE/DOCKET NUMBER: 230/107
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (213) 489-1600
;; TELEFAX: (213) 955-0440
;; TELEX: 67-3510
;; INFORMATION FOR SEQ ID NO: 1042:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 27 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; FEATURE:
;; OTHER INFORMATION: The letter "N" stands for the stem
;; OTHER INFORMATION: II region of a HH ribozyme.
US-08-985-162-1042

Query Match 61.0%; Score 12.2; DB 3; Length 27;
Best Local Similarity 55.6%; Pred. No. 1.2e+03;
Matches 10; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 3 tgatgcttaaaagcttac 20
: || | | | | | | | |
Db 10 UGAUGANGAAAAAGCUUC 27

RESULT 15
US-08-964-268-13/c
; Sequence 13, Application US/08964268
; Patent No. 6114503
; GENERAL INFORMATION:
; APPLICANT: WEI, YING-FEI
; APPLICANT: RUBEN, STEVEN M
; APPLICANT: SANCAR, AZIZ
; APPLICANT: HSU, SHIAO-WEN D
; APPLICANT: KAZANTSEV, ALEKSEY G
; TITLE OF INVENTION: HUMAN BLUE-LIGHT PHOTORECEPTOR HCRY2
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, NW, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/964,268
; FILING DATE: HEREWITH
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/030,189
; FILING DATE: 04-NOV-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.0750001/EKS
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-964-268-13

Qy 2 atgatgcttaaaagctt 18
| | | | | | | | | |
Db 20 AGGATGCCTGAAAGCTT 4

Search completed: October 2, 2001, 16:03:53
Job time: 14597 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 2, 2001, 16:18:45 ; Search time 876.95 seconds
(without alignments)
14.320 Million cell updates/sec

Title: US-09-757-100B-20

Perfect score: 20

Sequence: 1 catgatgcttaaaagcttac 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 730101 seqs, 313950809 residues

Total number of hits satisfying chosen parameters: 854978

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	22	AAC65552 Human focal adhesi
2	16.4	82.0	26	22	AAF81601 Bacterial 16S rRNA
3	15	75.0	15	22	AAC65572 Human focal adhesi
4	14.2	71.0	29	21	AAZ38455 Helicobacter pylori
5	13.8	69.0	27	20	AAZ221085 Staphylococcus aur
6	13.8	69.0	29	14	AAQ42521 Anti-sense strand
7	13.6	68.0	48	19	AAV43258 Primer used to amp
8	13.4	67.0	44	17	AAZ39690 CAMP receptor prot
9	13.2	66.0	20	17	AAZ27603 Anti-metastatic fu
10	13.2	66.0	20	17	AAZ12926 Human serum albumi
11	13.2	66.0	22	21	AAZ50168 3'PCR primer for i

c	12	13.2	66.0	33	16	AAT00817	5' 75 kd TNF recep
c	13	13.2	66.0	33	20	AAZ25353	Mouse A1 T cell re
c	14	13.2	66.0	40	21	AAZ56045	Plasmid pLAC11-rec
c	15	13	65.0	32	21	AAZ50654	Human HNRCP PCR pr
c	16	12.8	64.0	27	18	AAZ67579	Human flt1 VEGF re
c	17	12.8	64.0	32	18	AAZ49498	FokI cleavage doma
c	18	12.8	64.0	34	19	AAZ33065	Human tissue facto
c	19	12.8	64.0	34	20	AAZ78677	Ribozyme vector ol
c	20	12.8	64.0	36	20	AAZ78691	Plasmid insert pGE
c	21	12.8	64.0	42	20	AAZ78693	Ribozyme vector ol
c	22	12.8	64.0	42	20	AAZ78676	Ribozyme vector ol
c	23	12.8	64.0	42	20	AAZ78675	Ribozyme vector ol
c	24	12.6	63.0	27	18	AAZ70589	Human KDR VEGF rec
c	25	12.6	63.0	27	18	AAZ67769	Human flt1 VEGF re
c	26	12.6	63.0	30	21	AAZ11245	Primer p4 for anne
c	27	12.6	63.0	31	21	AAZ00870	3' primer to gener
c	28	12.6	63.0	31	21	AAZ00874	AAV2/4 bottom prim
c	29	12.6	63.0	35	18	AAZ62943	Primer for DNA enc
c	30	12.6	63.0	36	19	AAZ39935	Streptococcus pneu
c	31	12.6	63.0	36	19	AAZ01477	Prion protein forw
c	32	12.6	63.0	36	19	AAZ01479	Prion protein forw
c	33	12.6	63.0	36	22	AAZ59530	Mouse prion protei
c	34	12.6	63.0	36	22	AAZ59532	Human prion protei
c	35	12.6	63.0	50	20	AAZ52031	Synthetic plasmid
c	36	12.4	62.0	20	22	AAZ62919	Human PEPCK-cytoso
c	37	12.2	61.0	19	18	AAZ69751	Corn starch branch
c	38	12.2	61.0	19	21	AAZ82839	cdk4 ribozyme bind
c	39	12.2	61.0	19	21	AAZ82840	cdk4 ribozyme bind
c	40	12.2	61.0	19	21	AAZ82841	cdk4 ribozyme bind
c	41	12.2	61.0	25	21	AAZ34652	Human growth facto
c	42	12.2	61.0	27	18	AAZ70719	Human KDR VEGF rec
c	43	12.2	61.0	27	18	AAZ68287	Human flt1 VEGF re
c	44	12.2	61.0	27	19	AAZ98262	Human EGF-R hamme
c	45	12.2	61.0	27	19	AAZ43570	Human blue-light p

ALIGNMENTS

RESULT 1

AAC65552
ID AAC65552 standard; DNA; 20 BP.
XX
AC AAC65552;
XX
XX
DT 12-FEB-2001 (first entry)
XX
DE Human focal adhesion kinase antisense sequence #18.
XX
KW Human; focal adhesion kinase; FAK; signal transduction; cancer;
KW embryonic development disorder; angiogenic disorder; wound healing;
KW antisense; phosphothioate; ss.
XX
OS Homo sapiens.
XX
PN US6133031-A.
XX
PD 17-OCT-2000.
XX
PF 19-AUG-1999; 99US-0377310.
XX
PR 19-AUG-1999; 99US-0377310.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Monia BP, Gaarde WA;
XX
DR WPI; 2001-006141/01.
XX
PT New antisense compounds for inhibiting focal adhesion kinase
PT expression, especially useful for inhibiting retinal
PT neovascularization, or for diagnosing and treating e.g. colon cancer -
XX

PS Claim 3; Column 23; 30pp; English.

XX The present invention describes a number of phosphorothioate antisense
 CC sequences to the human focal adhesion kinase (FAK) protein. This protein
 CC is involved in integrin-mediated signal transduction, and is implicated
 CC in cancer, particularly colon, breast and oral tumours, embryonic
 CC development disorders, angiogenic disorders and wound healing. The
 CC antisense sequences, including the one shown here, can be used in the
 CC treatment of all of these.

XX Sequence 20 BP; 7 A; 4 C; 3 G; 6 T; 0 other;

Query Match 100.0%; Score 20; DB 22; Length 20;

Best Local Similarity 100.0%; Pred. No. 0.73;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 catgatgcttaaaagcttac 20

|||||

Db 1 catgatgcttaaaagcttac 20

RESULT 2

AAF81601/c
 ID AAF81601 standard; DNA; 26 BP.

AC AAF81601;

XX 05-JUN-2001 (first entry)

DE Bacterial 16S rRNA coding sequence PCR primer RVR-3.

XX Probe; PCR primer; 16S rRNA; bacterial detection; Microbispora;

KW Microtetraspora; Nonomuria; Planobispora; ss.

XX Microbispora.

OS Microtetraspora.

OS Planobispora.

XX WO200123608-A2.

XX 05-APR-2001.

PF 25-SEP-2000; 2000WO-EP09459.

XX 27-SEP-1999; 99US-0156171.

XX (MERI) MERCK SHARP & DOHME ESPANA SAE.

PA Genilloud O, Mellado RP, Parro V, Rodriguez V;

PI WPI; 2001-281685/29.

XX Novel nucleic acid probe hybridizing to nucleic acid encoding portion
 PT of 16S rRNA of bacteria of genera Microbispora, Microtetraspora,
 PT Nonomuria and Planobispora, useful for detecting these bacteria in
 PT sample -

XX Disclosure; Page 9; 20pp; English.

PS The present invention provides several probes and PCR primers which can
 CC be used in the detection of bacteria belonging to the genera of
 CC Microbispora, Microtetraspora, Nonomuria and Planobispora. The sequences
 CC hybridise to the 16S rRNA coding sequence of the organism. The present
 CC sequence is a PCR primer of the invention.

XX Sequence 26 BP; 7 A; 8 C; 5 G; 6 T; 0 other;

Query Match

Best Local Similarity 82.0%; Score 16.4; DB 22; Length 26;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 catgatgcttaaaagctt 18

|||||

Db 18 CATGTTGCTTAAAGCTT 1

RESULT 3

AAC65572

ID AAC65572 standard; DNA; 15 BP.

XX AAC65572;

XX 12-FEB-2001 (first entry)

XX Human focal adhesion kinase antisense sequence #38.

XX Human; focal adhesion kinase; FAK; signal transduction; cancer;

KW embryonic development disorder; angiogenic disorder; wound healing;

KW antisense; phosphorothioate; ss.

XX Homo sapiens.

XX US6133031-A.

XX 17-OCT-2000.

XX 19-AUG-1999; 99US-0377310.

PR 19-AUG-1999; 99US-0377310.

XX (ISIS-) ISIS PHARM INC.

XX Monia BP, Gaarde WA;

XX WPI; 2001-006141/01.

XX New antisense compounds for inhibiting focal adhesion kinase

PT expression, especially useful for inhibiting retinal

PT neovascularization, or for diagnosing and treating e.g. colon cancer -

PS Example 2; Column 25; 30pp; English.

XX The present invention describes a number of phosphorothioate antisense
 CC sequences to the human focal adhesion kinase (FAK) protein. This protein
 CC is involved in integrin-mediated signal transduction, and is implicated
 CC in cancer, particularly colon, breast and oral tumours, embryonic
 CC development disorders, angiogenic disorders and wound healing. The
 CC antisense sequences, including the one shown here, can be used in the
 CC treatment of all of these.

XX Sequence 15 BP; 5 A; 2 C; 3 G; 5 T; 0 other;

Query Match 75.0%; Score 15; DB 22; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.8e+02;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 tgatgcttaaaagct 17

|||||

Db 1 tgatgcttaaaagct 15

RESULT 4

AAZ38455/c

ID AAZ38455 standard; DNA; 29 BP.

XX AAZ38455;

XX 22-FEB-2000 (first entry)

XX Helicobacter pylori neutrophil activating protein (NAP) PCR primer #2.

XX Neutrophil activating protein; NAP; stomach; ulcer; cancer; neutrophil;
 KW activation; adhesion; inflammatory response; inflammation;

KW cloning artefact; salting out; ammonium sulphate;
 KW metal chelate chromatography; therapy; diagnosis; therapeutic agent;
 KW vaccine; immunoassay; immunodiagnosis; PCR; primer; ss.
 XX
 OS Synthetic.
 OS Helicobacter pylori.
 XX
 PN WO9953310-A1.
 XX
 PD 21-OCT-1999.
 XX
 PF 07-APR-1999; 99WO-IB00695.
 XX
 PR 08-APR-1998; 98GB-0007721.
 XX
 PA (CHIR-) CHIRON SPA.
 XX
 PI Grandi G;
 XX
 DR WPI; 2000-052659/04.
 XX
 PS Enriching presence of Helicobacter pylori neutrophil activating
 PT protein, useful in diagnostic and therapeutic products and processes
 PT
 XX Disclosure; Page 8; 26pp; English.
 XX
 CC This sequence represents NAP PCR primer #2, used with primer #1
 CC (AAZ38454) to amplify DNA (AAZ38453) encoding the neutrophil activating
 CC protein (NAP) from Helicobacter pylori strain CCUG. The PCR product
 CC was then cloned into the Escherichia coli and Bacillus subtilis
 CC shuttle vector pSM214G for recombinant production. In humans
 CC infected with H. pylori, NAP promotes activation and adhesion
 CC of neutrophils to endothelial cells, an inflammatory response.
 CC Since H. pylori is responsible for stomach inflammation, it is possible
 CC that NAP elicits the inflammatory response, probably at an early stage
 CC of gastric ulcer disease, when neutrophils accumulate in the superficial
 CC gastric mucosa. The invention relates to a novel process for enriching
 CC the presence of Helicobacter pylori NAP in a mixture of proteins. This
 CC comprises the steps of salting out other proteins (NAP being soluble at
 CC 80% ammonium sulphate saturation) and metal chelate chromatography
 CC (preferably with immobilised nickel cations). The NAP purified or
 CC enriched in this way is free from amino acid sequences or alterations
 CC introduced during cloning (e.g., polyhistidine tags, thioredoxin fusions
 CC or GST fusions). NAP produced via this process may be useful for the
 CC production of therapeutic agents, such as vaccines. It may also be
 CC useful in an immunoassay to ascertain antibody levels in a body sample,
 CC and in immunodiagnosis kits.
 XX
 SQ Sequence 29 BP; 8 A; 8 C; 4 G; 9 T; 0 other;
 XX
 Query Match 71.0%; Score 14.2; DB 21; Length 29;
 Best Local Similarity 84.2%; Pred. No. 4.6e+02;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 catgatgcttaaaagctta 19
 ||| |||||
 Db 23 CATTTGGCTTAAAGCTTA 5
 RESULT 5
 AAZ21085/c
 ID AAZ21085 standard; DNA; 27 BP.
 XX
 AC AAZ21085;
 XX
 DT 17-NOV-1999 (first entry)
 XX
 DE Staphylococcus aureus trxB PCR primer #2.
 XX
 KW Staphylococcus; trxB; thioredoxin reductase; antimicrobial;
 KW PCR primer; ss.
 XX

OS Synthetic.
 OS Staphylococcus aureus.
 XX
 PN WO9945123-A1.
 XX
 PD 10-SEP-1999.
 XX
 PF 02-MAR-1999; 99WO-US04512.
 XX
 PR 02-MAR-1998; 98US-0076525.
 XX
 PA (ABBO) ABBOTT LAB.
 XX
 PI Aharonowitz Y, Borovok I, Cohen G, Uziel O, Katz L;
 XX
 DR WPI; 1999-551044/46.
 XX
 PT A new thioredoxin reductase from Staphylococcus aureus
 XX
 PS Example 3; Page 32; 59pp; English.
 XX
 CC The present invention describes Staphylococcus thioredoxin reductase
 CC (trxB). The present sequence represent a PCR primer for S. aureus trxB.
 CC trxB inhibitors can be used as antimicrobials to treat a Staphylococcus,
 CC particularly S. aureus, infection. trxB inhibitors are antimicrobials to
 CC which, unlike most of those in the prior art, Staphylococcus has not yet
 CC developed a resistance.
 XX
 SQ Sequence 27 BP; 7 A; 6 C; 4 G; 10 T; 0 other;
 XX
 Query Match 69.0%; Score 13.8; DB 20; Length 27;
 Best Local Similarity 88.2%; Pred. No. 7.2e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 2 atgatgcttaaaagctt 18
 ||| |||||
 Db 20 ATCAAGCTTAAAGCTT 4
 RESULT 6
 AAQ42521/c
 ID AAQ42521 standard; DNA; 29 BP.
 XX
 AC AAQ42521;
 XX
 DT 27-SEP-1993 (first entry)
 XX
 DE Anti-sense strand of the coding sequence of human 7B2.
 XX
 KW 7B2; chaperone function; deaggregation; PCR; ss.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT CDS complement (9..29)
 FT /*tag= a
 XX
 PN WO9311248-A.
 XX
 PD 10-JUN-1993.
 XX
 PF 27-NOV-1992; 92WO-EP02740.
 XX
 PR 29-NOV-1991; 91NL-0002009.
 XX
 PA (DYKA-) UNIV STICHTING KATHOLIEKE.
 PA (CIBA) CIBA GEIGY AG.
 XX
 PI Martens GJM, Chaudhuri B, Stephan C;
 XX
 DR WPI; 1993-197066/24.
 XX

PT Efficient expression and de-aggregation of protein - by treating
PT co-expressing protein, e.g. hormone, growth or coagulation factor
PT or neuro-peptide with 7B2
XX
PS Example; Page 36; 41pp; English.
XX
CC The source of the DNA is partly human genomic DNA whilst the
CC immediate experimental source is synthetic. AAQ42515 and AAQ42521 are
CC used in the construction of a truncated 7B2 gene encoding an
CC amino terminal 7B2 signal peptide and the first 170 AAs of the
CC human protein. They are used as primers in a PCR using complete
CC human cDNA.
XX
SQ Sequence 29 BP; 11 A; 6 C; 3 G; 9 T; 0 other;

Query Match 69.0%; Score 13.8; DB 14; Length 29;
Best Local Similarity 88.2%; Pred. No. 7.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 tgatgcttaaaagctta 19
|| ||| ||||| |||||
Db 18 TGTGCTATAAAGCTTA 2

RESULT 7
AAV43258
ID AAV43258 standard; DNA; 48 BP.
XX
AC AAV43258;
XX
DT 27-OCT-1998 (first entry)
XX
DE Primer used to amplify plasmid pK5DT.
XX
KW Non-covalent complex; antibody; immunoglobulin; immunogen; vaccine;
KW cytotoxic; expression agent; treatment; cancer; expression; transgene;
KW primer; ss.
XX
OS Synthetic.
XX
PN WO9834956-A1.
XX
PD 13-AUG-1998.
XX
PF 06-FEB-1998; 98WO-FR00227.
XX
PR 07-FEB-1997; 97FR-0001420.
XX
PA (COMS) COMMISSARIAT ENERGIE ATOMIQUE.
XX
PI Drevet P, Leonetti M, Menez A;
XX
DR WPI; 1998-447169/38.
XX
PT New non-covalent complex of targeting antibody and immunoglobulin
PT binding component - linked to active agent, e.g. antigen, drug or
PT nucleic acid, used for treatment of cancer
XX
PS Example 6; Page 20; 42pp; French.
XX
CC AAV43257-58 represent primers used to amplify plasmid pK5DT. The
CC specification describes a non-covalent complex that comprises at
CC least one antibody, or its fragments, able to bind a cell-surface
CC molecule and a component that binds (to only 1 type of site) an
CC immunoglobulin (Ig) or fragment, and is associated with an active
CC substance. The complexes are used as immunogens, vaccines or as
CC cytotoxic or expression agents, e.g. for treatment of cancer or
CC for expressing transgenes.
XX
SQ Sequence 48 BP; 14 A; 9 C; 10 G; 15 T; 0 other;

Query Match 68.0%; Score 13.6; DB 19; Length 48;
Best Local Similarity 80.0%; Pred. No. 9.3e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 catgatgcttaaaagcttac 20
|| ||| ||||| |||||
Db 8 caggatccttataagcttcc 27

RESULT 8
AAT39690
ID AAT39690 standard; DNA; 44 BP.
XX
AC AAT39690;
XX
DT 04-APR-1997 (first entry)
XX
DE CAMP receptor protein DNA, PCR primer.
XX
KW Green fluorescent protein; detection; active substance; affecting;
KW intracellular process; fluorescence; probe; screen; identification;
KW luminescent; real time; study; second messenger; enzyme; primer;
KW protein kinase; PCR; polymerase chain reaction; CAMP; receptor;
KW protein; ss.
XX
OS Synthetic.
XX
PN WO9623898-A1.
XX
PD 08-AUG-1996.
XX
PF 31-JAN-1996; 96WO-DK00052.
XX
PR 07-SEP-1995; 95DK-0000982.
PR 31-JAN-1995; 95DK-0000110.
XX
PA (NOVO) NOVO-NORDISK AS.
XX
PI Bjorn SP, Poulsen LK, Thastrup O, Tullin S;
XX
DR WPI; 1996-371444/37.
XX
PT New construct encoding modified green fluorescent protein - contg.
PT e.g. enzyme recognition site, useful for detecting biologically
PT active substances affecting intracellular processes
XX
PS Example 3; Page 20; 48pp; English.
XX
CC A claimed fusion construct containing sequences encoding the
CC Aequorea victoria green fluorescent protein (GFP) and a portion of
CC the CAMP receptor protein, i.e. a sequence PCR amplified using the
CC PCR primer pair AAT39689/90, can be used for the detection of a
CC biologically active substance affecting intracellular processes.
CC A cell containing the construct is cultured under conditions
CC permitting GFP expression, and its fluorescence measured. The cell
CC is then incubated with the substance, and its fluorescence
CC measured, where any change indicates that the substance is
CC biologically active. The construct can also be used to generate
CC probes for use in basic research, and screening programmes to
CC identify new biologically active substances. The use of
CC luminescent probes allows real time studies of 2nd messengers and
CC specific enzymes, e.g. protein kinases, in single living cells,
CC making possible the study of the precise timing and spatial
CC characteristics of these factors. Due to the strong fluorescence
CC of GFP, the luminescence of cells expressing the probes, which
CC are easily introduced into cells, can be easily detected and
CC analysed.
XX
SQ Sequence 44 BP; 12 A; 8 C; 11 G; 13 T; 0 other;

Query Match 67.0%; Score 13.4; DB 17; Length 44;
Best Local Similarity 93.3%; Pred. No. 1.2e+03;

	Matches	14;	Conservative	0;	Mismatches	1;	Indels	0;	Gaps	0;
Qy	5	atgcttaaaagctta	19							
Db	5	atcttaaaagctta	19							

RESULT	9
AA27603/c	
ID	AA27603 standard; DNA; 20 BP.
XX	
AC	AA27603;
XX	
DT	03-SEP-1996 (first entry)
XX	
DE	Anti-metastatic fusion protein-encoding vector construction primer.

PT Fusion protein comprising human serum albumin contg. peptide
PT inserted at arbitrary position - useful for, e.g. inhibiting cancer
PT metastasis
XX
PS Example 5; Page 21; 24pp; Japanese.

Query Match	66.0%	Score 13.2;	DB 17;	Length 20;
Best Local Similarity	83.3%;	Pred. No. 1.4e+03;		
Matches 15;	Conservative 0;	Mismatches 3;	Indels 0;	Gaps 0;

RESULT 10	
AAT12926/C	
ID	AAT12926 standard; DNA; 20 BP.
XX	
XX	
XX	AAT12926;
XX	
XX	
XX	23-AUG-1996 (first entry)
XX	
XX	Human serum albumin gene PCR primer.

XX	HSA; modif; mutagenesis; genetic engineering; fusion gene;
KW	restriction endonuclease; recognition site; amplification;
KW	polymerase chain reaction; ss.
XX	
OS	Synthetic.
XX	
PN	JP08051982-A.
XX	
PD	27-FEB-1996.
XX	
PF	11-AUG-1994; 94JP-0209369.
XX	
PR	11-AUG-1994; 94JP-0209369.
XX	
PA	(ASAG) ASahi GLASS CO LTD.
XX	
WI	WPI; 1996-174566/18.
XX	
PT	Human serum albumin gene modified by introduction of restriction
PT	site - useful for production of fusion proteins by inserting active
PT	peptide coding sequence into new restriction site
XX	
PS	Example 2 and 3; Page 17; 19pp; Japanese.

Restriction enzyme recognition sites are introduced into the human serum albumin gene at one or more positions to facilitate preparation of fusion genes. The restriction sites are pref. introduced at the N-terminus, the C-terminus, between the first and second domains and/or between the second and third domains of HSA. The modified HSA gene can then readily be fused to a sequence coding for a physiologically active peptide, e.g. a cancer metastasis inhibitor. The present sequence is that of a PCR primer which was used in the construction of coding sequences AAL12919 and AAL12920 which had restriction sites introduced into the gene at positions corresp. to the region between domains 1 and 2 or between domains 2 and 3, respectively.

Sequence 20 BP; 6 A; 3 C; 2 G; 9 T; 0 other;

Query Match	66.0%	Score 13.2;	DB 17;
Best Local Similarity	83.3%	Pred. No. 1.4e+03;	Length 20;
Matches 15;	Conservative	0;	Mismatches 3;
			Indels 0;
			Gaps 0;

RESULT 11
AAZ50168/c
ID AAZ50168 standard; DNA; 22 BP.

04-MAY-2000 (first entry)
3'PCR primer for isolation and characterisation of *P. pastoris* FLD1 gene.
Methylotrophic yeast; formaldehyde dehydrogenase 1; FLD1; marker;
formaldehyde resistance; PCR primer; ss.
KW

XX	
PF	02-JUL-1999; 99WO-US15016.
XX	
PR	03-JUL-1998; 98US-0091699.

```

PA (RESE ) RESEARCH CORP TECHNOLOGIES INC.
XX
PI Cregg JW;
XX
XX WPI; 2000-182118/16.
XX
XX New formaldehyde dehydrogenase gene for methylotrophic yeast, useful as
PT selection marker, also its promoter for regulated expression of
PT heterologous polypeptides
XX
XX Example 2; Page 46; 101pp; English.
XX
XX The present sequence is a 3' PCR primer used in RT-PCR to amplify
CC intron corresponding region from total P. pastoris mRNA, for isolation
CC and characterisation of formaldehyde dehydrogenase 1 (FLD1) gene. FLD
CC protects cells from toxic effects of formaldehyde and imparts
CC formaldehyde resistance. It is therefore useful as a selectable marker
CC in methylotrophic yeast. Expression cassettes comprising FLD regulatory
CC sequences (promoter and terminator) can be used to control the
CC expression of heterologous proteins in transformed methylotrophic
CC yeast cells. Formaldehyde resistant host cells can be selected by
CC transforming them with a vector comprising FLD gene operably linked to
CC a heterologous promoter and growing them in the presence of formaldehyde.
XX
XX Sequence 22 BP; 8 A; 5 C; 6 G; 3 T; 0 other;
SQ

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Query Match 66.0%; Score 13.2; DB 21; Length 22;
Best Local Similarity 83.3%; Pred. No. 1.4e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 tgatgcttaaaagcttac 20
Db 21 TGATGCTTACACGCTTTC 4

RESULT 12
AAT00817/c
ID AAT00817 standard; DNA; 33 BP.
AC AAT00817;
XX
XX 13-MAY-1996 (first entry)
DT
DE 5' 75 kD TNF receptor primer.
DE
KW Tumour necrosis factor; TNF; erythropoietin receptor; EpoR; cytokine;
KW tumour therapy; polymerase chain reaction; PCR; primer; amplify; ss.
XX
XX Synthetic.
XX
XX WO9526985-A1.
PN
XX 12-OCT-1995.
PD
XX 05-APR-1995; 95WO-US04221.
PF
XX 05-APR-1994; 94US-0224593.
PR
XX (TEXA ) UNIV TEXAS SYSTEM.
PA
XX Bazzoni FM, Beutler BA;
PI
XX WPI; 1995-358585/46.
XX
XX New constructs for stimulating signalling in cells - comprising a
PT cytokine receptor cytoplasmic domain linked to a multimerising
PT extracellular domain
XX
XX Example 5; Page 16; 42pp; English.
PS
XX AAT00817 and AAT00818 are amplification primers for the stem,
XX transmembrane and cytoplasmic domains of the 75 kD tumour necrosis factor
CC

```

```

(TNF) receptor. AAT00815 and AAT00816 amplify the 55 kD TNF receptor.
CC The amplified sequence is used in a chimeric protein with the
CC erythropoietin receptor (EpoR) sequence amplified by AAT00813 and
CC AAT00814. A vector that expresses a chimeric receptor, such as the one
CC created using the amplified sequence, can be used to induce a cytotoxic
CC effect in a cell. The chimeric receptor can be used for the treatment of
CC tumours, and to provide a model for studying the formation of tumours.
CC By altering the extracellular and transmembrane domains of the chimeric
CC protein, the target sequence is changed. The formation of multimeric
CC receptor complexes on the extracellular surface, when the chimeric
CC protein is used, is sufficient for transmitting a positive signal to the
CC cytoplasmic domain of the receptor. This occurs even in the absence of
CC the cognate ligand, or in the presence of a ligand that has entirely
CC different activities. The advantage with using the chimeric protein is
CC that the response of the cytokine (in this case TNF) can be induced
CC without side effects.
XX
XX Sequence 33 BP; 8 A; 10 C; 6 G; 9 T; 0 other;
SQ

```

```

Query Match 66.0%; Score 13.2; DB 16; Length 33;
Best Local Similarity 83.3%; Pred. No. 1.4e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 atgatgcttaaaagctta 19
Db 23 AGGATGCTTGAAGCTTA 6

RESULT 13
AAX25353
ID AAX25353 standard; DNA; 33 BP.
XX
XX AC AAX25353;
XX
XX 19-JUL-1999 (first entry)
DT
DE Mouse A1 T cell receptor beta chain PCR primer.
DE
KW T cell receptor beta chain; mouse; transgenic animal;
KW animal model; immunological tolerance; graft rejection;
KW tissue grafting; neonatal intolerance; transplantation antigen;
KW H-Y antigen; PCR; primer; ss.
XX
XX Synthetic.
XX
XX OS Mus musculus.
XX
XX WO9916867-A1.
PN
XX PD 08-APR-1999.
XX
XX PF 30-SEP-1998; 98WO-GB02965.
XX
XX PR 01-OCT-1997; 97GB-0020888.
XX
XX PA (ISIS-) ISIS INNOVATION LTD.
XX
XX PI Cobbold SP, Waldmann H, Zelenika D;
XX
XX DR WPI; 1999-255090/21.
XX
XX Transgenic non-human mammal having only CD4 positive T cells
PT specific for at least one transplantation antigen, useful for
PT studying immunological tolerance
XX
XX Example 1; Page 9; 41pp; English.
PS
XX This oligonucleotide was used as a primer for the PCR amplification
CC of a cDNA clone (see AAX25358) coding for the T cell receptor (TCR)
CC beta chain (see AAY05728) from the A1 CD4+ T cell clone isolated
CC from CBA/Ca mice. The A1 clone recognises the minor
CC histocompatibility antigen H-Y present in male, but absent in
CC female, mice. The amplified product was used in the construction
CC

```

CC of Al(M) transgenic mice. The invention relates to a transgenic
 CC animal model comprising TCR alpha and beta chains. It provides a
 CC genetically modified non-human mammal having a population of CD4
 CC positive T cells specific for one or a limited number of selected
 CC antigens, including at least transplantation antigen capable of
 CC rejecting a tissue transplant containing the transplantation
 CC antigen and, if applicable, the other selected antigens. The
 CC animal has TCR genes which encode a TCR specific for the
 CC transplantation antigen. The animal is useful for studying
 CC immunological tolerance, especially the mechanisms of tolerance to,
 CC and the rejection of, tissue grafts, and in pregnancy. The animals
 CC are also useful for testing agents for biological activity in
 CC promoting or reducing immunological tolerance.
 XX
 SQ Sequence 33 BP; 10 A; 5 C; 9 G; 9 T; 0 other;
 Query Match 66.0%; Score 13.2; DB 20; Length 33;
 Best Local Similarity 83.3%; Pred. No. 1.4e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 catgatgcttaaaagctt 18
 Db 8 caggatgcataaaagattt 25
 RESULT 14
 ID AAA56045/c
 XX AAA56045 standard; DNA; 40 BP.
 AC AAA56045;
 XX
 DT 05-SEP-2000 (first entry)
 XX
 DE Plasmid pLAC11-recA construction PCR primer SEQ ID NO:17.
 XX
 KW Escherichia coli; E. coli; randomised peptide library; identification;
 KW stabilised bioactive peptide; synthesis; intracellular selection;
 KW screening; lac operon; protease resistant; peptidase resistant;
 KW Rop protein; glutathione sulphotransferase; thioredoxin; infection;
 KW maltose binding protein; glutathione reductase; antimicrobial;
 KW antibacterial; PCR primer; ss.
 XX
 OS Escherichia coli.
 OS Synthetic.
 XX
 XX W0200022112-A1.
 PN
 XX
 PD 20-APR-2000.
 XX
 XX 12-OCT-1999; 99WO-US23731.
 XX
 XX 13-OCT-1998; 98US-0104013.
 PR
 PR 14-DEC-1998; 98US-0112150.
 XX
 XX (UYGE-) UNIV GEORGIA RES FOUND INC.
 PA (ALTM/) ALTMAN E.
 PA
 XX Altman E.
 PI
 XX
 DR WPI; 2000-317972/27.
 XX
 XX Identifying recombinantly an antimicrobial bioactive peptide used as a
 PT therapeutic agent involves transforming a host cell with expression
 PT vector with tightly regulable control region and measuring its
 PT inhibition.
 XX
 PS Example 1; Page 36; 135pp; English.
 XX
 CC The present invention describes a method for identifying a bioactive
 CC peptide (BP) involving transforming a cell with an expression vector
 CC comprising a tightly regulatable control region operably linked to a
 CC nucleic acid sequence encoding a peptide (P), growing the transformed

CC cell under conditions that repress expression of (P) and then inducing
 CC its expression which, if is inhibitory to host cell growth, is
 CC indicative of BP expression. An antimicrobial peptide from the present
 CC invention, which is stabilised, is used for treating a patient having a
 CC condition treatable with a peptide drug. The stabilised peptides are
 CC also used for inhibiting the growth of a microbe. The new antibacterial
 CC peptides are useful to treat various pathogenic bacteria such as
 CC Staphylococci, Streptococci and Enterococci which are the primary causes
 CC of nosocomial infections. Novel inhibitor peptides identified by the
 CC method can be medical treatments and therapies directed against
 CC microbial infection. Also, these novel inhibitor peptides can be used,
 CC in turn, to identify additional novel antibacterial peptides using a
 CC synthetic approach, and can also be used to elucidate potential new drug
 CC targets. The inhibitor peptide target which is inactivated is identified
 CC using reverse genetics by isolating mutants that are no longer inhibited
 CC by the peptide. These mutants are then mapped in order to precisely
 CC determine the protein target that is inhibited. AAA56033 to AAA56106 and
 CC AA990964 to AA990999 are sequences used in the exemplification of the
 CC present invention.
 XX
 SQ Sequence 40 BP; 12 A; 6 C; 5 G; 17 T; 0 other;
 Query Match 66.0%; Score 13.2; DB 21; Length 40;
 Best Local Similarity 83.3%; Pred. No. 1.4e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 2 atgatgcttaaaagctta 19
 Db 23 AAGATTTTAAAGCTTA 6
 RESULT 15
 ID AAA60654/c
 XX AAA60654 standard; DNA; 32 BP.
 AC AAA60654;
 XX
 DT 24-OCT-2000 (first entry)
 XX
 XX Human HNRCR PCR primer SEQ ID NO:26.
 DE
 XX Human; HNRCR; nuclear receptor coreceptor; PCR primer; ss.
 KW
 XX Homo sapiens.
 OS
 XX CML250094-A.
 PN
 XX
 PD 12-APR-2000.
 XX
 XX 06-OCT-1998; 98CN-0120919.
 PF
 XX 06-OCT-1998; 98CN-0120919.
 PR
 XX (XINH-) XINHUANGPU FUDAN GENE ENG CO LTD SHANGHA.
 PA
 XX Yu L, Tu Q, Zhao Y;
 PI
 XX WPI; 2000-400830/35.
 DR
 XX Preparation of new human kernon acceptor co-repressor coding series and
 PT the polypeptide -
 PT
 XX Example 3; Page 11; 58pp; Chinese.
 PS
 XX The present invention describes a human homologue of nuclear receptor
 CC coreceptor (HNRCR). The present sequence represents a PCR primer for
 CC human HNRCR, which is used in an example from the present invention.
 CC
 XX Sequence 32 BP; 11 A; 7 C; 8 G; 6 T; 0 other;
 SQ
 Query Match 65.0%; Score 13; DB 21; Length 32;

Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 tgcttaaaagctt 18
|||||
Db 17 TGCTTAAAGCTT 5

Search completed: October 2, 2001, 16:18:46
Job time: 15490 sec

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OM nucleic - nucleic search, using sw model

Run on: October 2, 2001, 16:03:52 ; Search time 417.38 Seconds
(without alignments)
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Title: US-09-757-100B-18

Perfect score: 20

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Searched: 324599 seqs, 94655562 residues

Total number of hits satisfying chosen parameters: 460742

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

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6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	%			
1	20	100.0	20	3	US-09-377-310-18	Sequence 18, Appl
2	15	75.0	15	3	US-09-377-310-38	Sequence 38, Appl
3	14.2	71.0	20	3	US-09-357-071-39	Sequence 39, Appl
4	12.8	64.0	25	3	US-08-763-428A-10	Sequence 10, Appl
5	12.8	64.0	29	1	US-08-306-871-32	Sequence 32, Appl
6	12.8	64.0	29	1	US-08-569-959-32	Sequence 32, Appl
C 7	12.6	63.0	35	1	US-08-469-005A-7	Sequence 7, Appl
C 8	12.4	62.0	26	3	US-08-938-885A-41	Sequence 41, Appl
9	12.4	62.0	30	1	US-08-463-975-4	Sequence 4, Appl
10	12.4	62.0	30	1	US-08-783-266-4	Sequence 4, Appl
11	12.4	62.0	30	2	US-02-023-327-4	Sequence 4, Appl
12	12.2	61.0	20	1	US-08-531-556-4	Sequence 4, Appl
13	12.2	61.0	20	1	US-08-472-416-4	Sequence 4, Appl
14	12.2	61.0	23	4	US-09-101-886B-30	Sequence 30, Appl
15	12.2	61.0	28	2	US-08-859-998-1026	Sequence 1026, Ap
16	12.2	61.0	33	2	US-08-479-275D-38	Sequence 38, Appl
17	12.2	61.0	33	2	US-08-488-271B-38	Sequence 38, Appl
C 18	12.2	61.0	34	2	US-08-612-840A-9	Sequence 9, Appl
19	12	60.0	20	3	US-09-377-310-43	Sequence 43, Appl
20	12	60.0	25	4	US-09-586-935-17	Sequence 17, Appl
21	12	60.0	40	2	US-08-685-576-11	Sequence 11, Appl
22	11.8	59.0	25	2	US-08-117-952-499	Sequence 499, App
23	11.8	59.0	35	4	US-08-957-621-3	Sequence 3, Appl
24	11.8	59.0	28	4	US-08-818-604-24	Sequence 24, Appl
C 25	11.8	59.0	38	2	US-08-857-946-106	Sequence 106, App
C 26	11.8	59.0	38	3	US-08-970-740-106	Sequence 106, App
C 27	11.8	59.0	38	4	US-09-262-773-45	Sequence 45, Appl

C	28	11.8	59.0	39	4	US-09-342-749-18	Sequence 18, Appl
	29	11.6	58.0	32	1	US-08-133-711-24	Sequence 24, Appl
C	30	11.6	58.0	32	1	US-08-276-852-15	Sequence 15, Appl
	31	11.6	58.0	32	1	US-08-133-011-22	Sequence 22, Appl
	32	11.6	58.0	32	1	US-08-322-730A-22	Sequence 22, Appl
	33	11.6	58.0	32	1	US-08-162-102C-3	Sequence 3, Appl
	34	11.6	58.0	32	1	US-08-387-874-22	Sequence 22, Appl
	35	11.6	58.0	32	1	US-08-899-575-15	Sequence 15, Appl
	36	11.6	58.0	32	1	US-08-899-575-15	Sequence 15, Appl
	37	11.6	58.0	32	2	US-08-383-619-22	Sequence 22, Appl
	38	11.6	58.0	32	4	US-08-907-739-22	Sequence 22, Appl
	39	11.6	58.0	32	5	PCI-US93-08364-22	Sequence 22, Appl
	40	11.6	58.0	32	5	PCI-US93-08786-3	Sequence 3, Appl
	41	11.6	58.0	32	5	PCI-US95-00067-3	Sequence 3, Appl
	42	11.6	58.0	32	5	PCI-US95-08743-15	Sequence 15, Appl
C	43	11.6	58.0	33	2	US-08-896-410-30	Sequence 30, Appl
C	44	11.6	58.0	38	1	US-08-276-852-20	Sequence 20, Appl
C	45	11.6	58.0	38	1	US-08-133-011-27	Sequence 27, Appl

ALIGNMENTS

```

RESULT      1
US-09-377-310-18
; Sequence 18, Application US/09377310B
; Patent No. 6133031
; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P.
; APPLICANT: Gaarde, William A.
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
; TITLE OF INVENTION: Expression
; FILE REFERENCE: ISPH-0389
; CURRENT APPLICATION NUMBER: US/09/377,310B
; CURRENT FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
US-09-377-310-18

```

Query Match	100.0%;	Score 20;	DB 3;	Length 20;
Best Local Similarity	100.0%;	Pred. No. 0.087;		

Qy 1 tttcaaccagatggtcattc 20
|||||
Db 1 tttcaaccagatggtcattc 20

```

RESULT      2
US-09-377-310-38
; Sequence 38, Application US/09377310B
; Patent No. 6133031
; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P.
; APPLICANT: Gaarde, William A.
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
; TITLE OF INVENTION: Exoression
; FILE REFERENCE: ISPH-0389
; CURRENT APPLICATION NUMBER: US/09/377,310B
; CURRENT FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 38
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence

```

FEATURE:
OTHER INFORMATION: antisense sequence
US-09-377-310-38

Query Match 75.0%; Score 15; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 tcaaccagatggtca 17
|||||

Db 1 tcaaccagatggtca 15

RESULT 3
US-09-357-071-39
Sequence 39, Application US/09357071
Patent No. 6043091
GENERAL INFORMATION:
APPLICANT: Brett P. Monia
APPLICANT: Lex M. Cowsett
TITLE OF INVENTION: ANTISENSE MODULATION OF LIVER GLYCOGEN PHOSPHORYLASE EXPRESSION
FILE REFERENCE: RTS-0074
CURRENT APPLICATION NUMBER: US/09/357,071
CURRENT FILING DATE: 1999-07-19
NUMBER OF SEQ ID NOS: 47
SEQ ID NO 39
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-09-357-071-39

Query Match 71.0%; Score 14.2; DB 3; Length 20;
Best Local Similarity 84.2%; Pred. No. 83;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ttccaaccagatggtcatt 19
|||

Db 1 ttccaaccagatggtcatt 19

RESULT 4
US-08-762-428A-10
Sequence 10, Application US/08762428A
Patent No. 6120993
GENERAL INFORMATION:
APPLICANT: Ye, Guo-jie
APPLICANT: Breslow, Esther M.
APPLICANT: Meister, Alton
TITLE OF INVENTION: 5-OXOPROLINASE
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON, HARGRAVE, DEVANS & DOYLE LLP
STREET: Clinton Square, P.O. Box 1051
CITY: Rochester
STATE: New York
COUNTRY: USA
ZIP: 14603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/762,428A
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: TIMIAN, SUSAN J.
REGISTRATION NUMBER: 34,103

REFERENCE/DOCKET NUMBER: 19603/1330
TELECOMMUNICATION INFORMATION:
TELEPHONE: 716-263-1636
TELEFAX: 716-263-1600
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-762-428A-10

Query Match 64.0%; Score 12.8; DB 3; Length 25;
Best Local Similarity 87.5%; Pred. No. 4.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ttcaaccagatggtca 17
|||||

Db 8 ttcaaccatattggca 23

RESULT 5
US-08-306-871-32
Sequence 32, Application US/08306871
Patent No. 5712118
GENERAL INFORMATION:
APPLICANT: Timothy F. Murphy
TITLE OF INVENTION: Vaccine For Branhameella catarrhalis
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hodgson, Russ, Andrews, Woods & Goodyear
STREET: 1800 One M&T Plaza
CITY: Buffalo
STATE: New York
COUNTRY: United States
ZIP: 14203-2391
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS/ Microsoft Windows 3.1
SOFTWARE: Wordperfect for Windows 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/306,871
FILING DATE: 20-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/129,719
FILING DATE: September 29, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Nelson, M. Bud
REGISTRATION NUMBER: 35,300
REFERENCE/DOCKET NUMBER: 11520.0053
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 856-4000
TELEFAX: (716) 849-0349
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single-stranded
TOPOLOGY: linear
ORIGINAL SOURCE:
ORGANISM: Branhameella catarrhalis
STRAIN: 25240
US-08-306-871-32

Query Match 64.0%; Score 12.8; DB 1; Length 29;
Best Local Similarity 87.5%; Pred. No. 4.6e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ttcaaccagatggtca 17

Db 10 TTCATCCAGATGATCA 25
 |||| ||||| |||

RESULT 6

US-08-569-959-32
 ; Sequence 32, Application US/08569959
 ; Patent No. 5725862
 ; GENERAL INFORMATION:
 ; APPLICANT: Timothy F. Murphy
 ; TITLE OF INVENTION: Vaccine For Branhamella catarrhalis
 ; NUMBER OF SEQUENCES: 52
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Hodgson, Russ, Andrews, Woods & Goodyear
 ; STREET: 1800 One M&T Plaza
 ; CITY: Buffalo
 ; STATE: New York
 ; COUNTRY: United States
 ; ZIP: 14203-2391
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: MS-DOS/ Microsoft Windows 3.1
 ; SOFTWARE: Wordperfect for Windows 5.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/569,959
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: U.S. 08/129,719
 ; FILING DATE: September 29, 1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Nelson, M. Bud
 ; REGISTRATION NUMBER: 35,300
 ; REFERENCE/DOCKET NUMBER: 11520.0053
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (716) 856-4000
 ; TELEFAX: (716) 849-0349
 ; INFORMATION FOR SEQ ID NO: 32:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 29 nucleotides
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single-stranded
 ; TOPOLOGY: linear
 ; ORGANISM: Branhamella catarrhalis
 ; STRAIN: 25240
 ; US-08-569-959-32

Query Match 64.0%; Score 12.8; DB 1; Length 29;
 Best Local Similarity 87.5%; Pred. No. 4.6e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ttcaaccagatggtca 17
 |||| ||||| |||
 Db 10 TTCATCCAGATGATCA 25

RESULT 7

US-08-469-005A-7/C
 ; Sequence 7, Application US/08469005A
 ; Patent No. 5665874
 ; GENERAL INFORMATION:
 ; APPLICANT: KUHAJDA, FRANCIS P.
 ; APPLICANT: PASTERNAK, GARY A.
 ; TITLE OF INVENTION: CANCER RELATED ANTIGEN
 ; NUMBER OF SEQUENCES: 14
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: BAKER & BOTTS, L.L.P.
 ; STREET: 1299 Pennsylvania Avenue, N.W.
 ; CITY: Washington
 ; STATE: DC

COUNTRY: USA
 ZIP: 20004-2400
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSeq Version 1.5
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/469,005A
 FILING DATE: 05-JUN-1995
 CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/188,426
 FILING DATE: 24-JAN-1994
 APPLICATION NUMBER: 08/096,908
 FILING DATE: 26-JUL-1993
 APPLICATION NUMBER: 07/917,716
 FILING DATE: 24-JUL-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Posorske, Laurence H
 REGISTRATION NUMBER: 34,698
 REFERENCE/DOCKET NUMBER: 062482-0113
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-639-7700
 TELEFAX: 202-639-7890
 TELEX:
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 35 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE:
 ORIGINAL SOURCE:
 US-08-469-005A-7

Query Match 63.0%; Score 12.6; DB 1; Length 35;
 Best Local Similarity 78.9%; Pred. No. 5.9e+02;
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 ttcaaccagatggtcattc 20
 ||||| ||||| |||||
 Db 35 TTCAGAAGATGGCCATGC 17

RESULT 8

US-08-938-835A-41/C
 ; Sequence 41, Application US/08938835A
 ; Patent No. 6060245
 ; GENERAL INFORMATION:
 ; APPLICANT: SORGE, Joseph A.
 ; APPLICANT: MULLINAX, Rebecca L.
 ; TITLE OF INVENTION: METHODS AND ADAPTORS FOR GENERATING
 ; TITLE OF INVENTION: SPECIFIC NUCLEIC ACID POPULATIONS
 ; NUMBER OF SEQUENCES: 69
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
 ; ADDRESSEE: Dunner, L.L.P.
 ; STREET: 1300 I Street, N.W.
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20005-3315
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/938,835A
FILING DATE: 26-SEPT-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/775,993
FILING DATE: 03-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/779,335
FILING DATE: 06-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Barker, M. Paul
REGISTRATION NUMBER: 32,013
REFERENCE/DOCKET NUMBER: 04121.0044-02000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-938-835A-41

Query Match 62.0%; Score 12.4; DB 3; Length 26;
Best Local Similarity 92.9%; Pred. No. 7.2e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 caaccagatgttca 17
|||||

Db 18 CAACGAGTGTGCA 5

RESULT 9
US-08-463-975-4
Sequence 4, Application US/08463975
Patent No. 5618717
GENERAL INFORMATION:
APPLICANT: WEI, ET AL.
TITLE OF INVENTION: HABH
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESSEE: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,975
FILING DATE: June 5, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/12058
FILING DATE: 21 OCT 1994
ATTORNEY/AGENT INFORMATION:
NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-331
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1744
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 BASE PAIRS

TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR
MOLECULE TYPE: Oligonucleotide
US-08-463-975-4

Query Match 62.0%; Score 12.4; DB 1; Length 30;
Best Local Similarity 92.9%; Pred. No. 7.4e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ttccaacagatgg 14
|||||

Db 9 TTTCATCCAGATGG 22

RESULT 10
US-08-783-266-4
Sequence 4, Application US/08783266
Patent No. 5747312
GENERAL INFORMATION:
APPLICANT: WEI, ET AL.
TITLE OF INVENTION: HABH
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESSEE: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/783,266
FILING DATE: 15-JAN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/463,975
FILING DATE: June 5, 1995
APPLICATION NUMBER: PCT/US94/12058
FILING DATE: 21 OCT 1994
ATTORNEY/AGENT INFORMATION:
NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-331
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 BASE PAIRS
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR
MOLECULE TYPE: Oligonucleotide
US-08-783-266-4

Query Match 62.0%; Score 12.4; DB 1; Length 30;
Best Local Similarity 92.9%; Pred. No. 7.4e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ttccaacagatgg 14
|||||

Db 9 TTTCATCCAGATGG 22

RESULT 11

```
US-09-023-327-4
; Sequence 4, Application US/09023327
; Patent No. 5929225
; GENERAL INFORMATION:
; APPLICANT: WEI, ET AL.
; TITLE OF INVENTION: HABH
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,327
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/463,975
; FILING DATE: June 5, 1995
; APPLICATION NUMBER: PCT/US94/12058
; FILING DATE: 21 OCT 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: FERRARO, GREGORY D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-331
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 BASE PAIRS
; TYPE: NUCLEIC ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: LINEAR
; MOLECULE TYPE: Oligonucleotide
US-09-023-327-4

Query Match 62.0%; Score 12.4; DB 2; Length 30;
Best Local Similarity 92.9%; Pred. No. 7.4e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ttcaaccagatgg 14
Db 9 TTTCATCCAGATGG 22

RESULT 12
US-09-531-556-4
; Sequence 4, Application US/08531556
; Patent No. 5776682
; GENERAL INFORMATION:
; APPLICANT: AgoulNIK, Alexander I
; APPLICANT: Kent First, Marijo
; APPLICANT: Muallem, Ariege
; TITLE OF INVENTION: MALE INFERTILITY Y-DELETION DETECTION
; TITLE OF INVENTION: BATTERY
; NUMBER OF SEQUENCES: 124
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dewitt Ross & Stevens, S.C.
; STREET: 8000 Excelsior Drive, Suite 401
; CITY: Madison
; STATE: WI
; COUNTRY: USA
; ZIP: 53717-1914

US-09-023-327-4
; Sequence 4, Application US/08472416
; Patent No. 5783390
; GENERAL INFORMATION:
; APPLICANT: AgoulNIK, A.
; APPLICANT: Kent, Marijo G.
; TITLE OF INVENTION: MALE INFERTILITY Y-DELETION DETECTION
; TITLE OF INVENTION: BATTERY
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dewitt Ross & Stevens, S.C.
; STREET: 8000 Excelsior Drive, Suite 401
; CITY: Madison
; STATE: WI
; COUNTRY: USA
; ZIP: 53717-1914
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/472,416
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sara, Charles S.
; REGISTRATION NUMBER: 30,492
; REFERENCE/DOCKET NUMBER: 34506.034
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 608-831-2100
; TELEFAX: 608-831-2106
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
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COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/531,556
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sara, Charles S.
; REGISTRATION NUMBER: 30,492
; REFERENCE/DOCKET NUMBER: 34506.034CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 608-831-2100
; TELEFAX: 608-831-2106
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-531-556-4

Query Match 61.0%; Score 12.2; DB 1; Length 20;
Best Local Similarity 82.4%; Pred. No. 8.9e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 ttcaaccagatggtcat 18
   ||| |||| |||||
Db 1 TCCATCCAGCTGGTCAT 17.

RESULT 13
US-08-472-416-4
; Sequence 4, Application US/08472416
; Patent No. 5783390
; GENERAL INFORMATION:
; APPLICANT: AgoulNIK, A.
; APPLICANT: Kent, Marijo G.
; TITLE OF INVENTION: MALE INFERTILITY Y-DELETION DETECTION
; TITLE OF INVENTION: BATTERY
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dewitt Ross & Stevens, S.C.
; STREET: 8000 Excelsior Drive, Suite 401
; CITY: Madison
; STATE: WI
; COUNTRY: USA
; ZIP: 53717-1914
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/472,416
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sara, Charles S.
; REGISTRATION NUMBER: 30,492
; REFERENCE/DOCKET NUMBER: 34506.034
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 608-831-2100
; TELEFAX: 608-831-2106
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
```

; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-472-416-4

Query Match 61.0%; Score 12.2; DB 1; Length 20;
Best Local Similarity 82.4%; Pred. No. 8.9e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 2 ttcaaccagatggtcat 18
| | | | | | | | | |
Db 1 TCCATCCAGCTGTCAT 17

RESULT 14

US-09-101-886B-30
; Sequence 30, Application US/09101886B
; Patent No. 6197507
; GENERAL INFORMATION:
; APPLICANT: BERG, THOMAS
; APPLICANT: TOLLERSRUD, OLE K
; APPLICANT: NILSSON, OIVIND
; TITLE OF INVENTION: GENETIC TEST FOR ALPHA-MANNOSIDOSIS
; NUMBER OF SEQUENCES: 104
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BARBARA G. ERNST
; STREET: 555 13TH STREET, NW SUITE 701E
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20004

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/101,886B
; FILING DATE: 29-JANUARY-1998
; CLASSIFICATION: 435

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB97/00109
; FILING DATE: 12-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: ERNST, BARBARA G
; REGISTRATION NUMBER: 30,377
; REFERENCE/DOCKET NUMBER: 1181-240
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-783-6040
; TELEFAX: 202-783-6031

INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "oligonucleotide"
; HYPOTHETICAL: NO
; ANTI-SENSE: YES
US-09-101-886B-30

Query Match 61.0%; Score 12.2; DB 4; Length 23;
Best Local Similarity 82.4%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 3 tcaaccagatggtcatt 19
| | | | | | | | | |
Db 6 TCATCCAGTTGTCAT 22

RESULT 15

US-08-859-998-1026
; Sequence 1026, Application US/08859998
; Patent No. 5994076
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Jokhadze, George
; APPLICANT: Bibilashvili, Robert
; TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1375
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 2200 Sand Hill Road, Suite 100
; CITY: Menlo Park
; STATE: CA
; COUNTRY: US
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/859,998
; FILING DATE: 21-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Field, Bret E.
; REGISTRATION NUMBER: 37,620
; REFERENCE/DOCKET NUMBER: 09096/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-322-5070
; TELEFAX: 415-854-0875
; INFORMATION FOR SEQ ID NO: 1026:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; OTHER INFORMATION: oligonucleotide primer
US-08-859-998-1026

Query Match 61.0%; Score 12.2; DB 2; Length 28;
Best Local Similarity 82.4%; Pred. No. 9.3e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 2 ttcaaccagatggtcat 18
| | | | | | | | | |
Db 3 TTCTACCAAGGTGTCAT 19

Search completed: October 2, 2001, 16:03:53
Job time: 14597 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 2, 2001, 16:18:45 ; Search time 876.95 Seconds
(without alignments)
14.320 Million cell updates/sec

Title: US-09-757-100B-18

Perfect score: 20

Sequence: 1 tttaaccagatggtcattc 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 730101 seqs, 313950809 residues

Total number of hits satisfying chosen parameters: 854978

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N_Geneseq_0601:*
1: /SIDS8/gcgdata/geneseq/geneseq/NA1980.DAT:*
2: /SIDS8/gcgdata/geneseq/geneseq/NA1981.DAT:*
3: /SIDS8/gcgdata/geneseq/geneseq/NA1982.DAT:*
4: /SIDS8/gcgdata/geneseq/geneseq/NA1983.DAT:*
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6: /SIDS8/gcgdata/geneseq/geneseq/NA1985.DAT:*
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9: /SIDS8/gcgdata/geneseq/geneseq/NA1988.DAT:*
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12: /SIDS8/gcgdata/geneseq/geneseq/NA1991.DAT:*
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20: /SIDS8/gcgdata/geneseq/geneseq/NA1999.DAT:*
21: /SIDS8/gcgdata/geneseq/geneseq/NA2000.DAT:*
22: /SIDS8/gcgdata/geneseq/geneseq/NA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	22	AAC65550 Human focal adhesi
2	15	75.0	15	22	AAC65570 Human focal adhesi
3	14.4	72.0	38	20	AA186411 Human liver glyco
4	14.2	71.0	20	21	AA14039 Maize polymorphic
5	13.8	69.0	41	19	AAV51245 Maize polymorphic
6	13.8	69.0	41	19	AAV51246 Maize polymorphic
7	13.8	69.0	41	19	AAV47956 Maize polymorphic
8	13.8	69.0	41	19	AAV47957 Maize polymorphic
9	13.4	67.0	41	19	AAV51243 Maize polymorphic
10	13.4	67.0	41	19	AAV51244 Maize polymorphic
11	13.4	67.0	41	19	AAV47954 Maize polymorphic

c 12	13.4	67.0	41	19	AAV47955	Maize polymorphic
c 13	13.2	66.0	33	21	AA255314	Neisseria species
c 14	13.2	66.0	50	20	AA252031	Synthetic plasmid
c 15	12.8	64.0	25	19	AAV28114	Rat 5-oxoprolinase
c 16	12.8	64.0	25	21	AA253025	Human beta-1,3-gal
c 17	12.8	64.0	25	21	AA253029	Human beta-1,3-gal
c 18	12.8	64.0	29	16	AA091896	B.cattarhalis CD e
c 19	12.8	64.0	29	21	AA04221	Polymorphic fragme
c 20	12.8	64.0	38	15	AA073036	Tyrosine-kinase sy
c 21	12.8	64.0	38	15	AA073037	Tyrosine-kinase sy
c 22	12.6	63.0	31	21	AA229977	PCR primer used in
c 23	12.6	63.0	35	18	AA188208	Probe used in prep
c 24	12.6	63.0	35	20	AA151118	Probe used to isol
c 25	12.6	63.0	35	20	AA03260	Probe used to isol
c 26	12.6	63.0	41	18	AA178192	Micro gene random
c 27	12.6	63.0	47	21	AA287025	RBP-7 biallelic ma
c 28	12.4	62.0	23	22	AA290273	Primer #17 used in
c 29	12.4	62.0	24	10	AA192881	ER-specific probe.
c 30	12.4	62.0	26	19	AA140115	PCR primer used to
c 31	12.4	62.0	30	17	AA129698	Primer for amplfy
c 32	12.4	62.0	30	18	AA168318	Human homologue of
c 33	12.4	62.0	30	20	AA188777	Human AlkB homolog
c 34	12.4	62.0	46	21	AA166377	Chitinase specific
c 35	12.4	62.0	46	21	AA172653	Chitinase degenera
c 36	12.2	61.0	20	18	AA172839	SPT6 homologue for
c 37	12.2	61.0	20	18	AA168289	Locl-specific prim
c 38	12.2	61.0	27	20	AA172185	Human NBC PCR prim
c 39	12.2	61.0	29	21	AA140437	Polymorphic fragme
c 40	12.2	61.0	30	20	AA172184	Human NBC PCR prim
c 41	12.2	61.0	30	21	AA188895	Human wolframin in
c 42	12.2	61.0	42	20	AA186407	PCR primer PDZK5.4
c 43	12	60.0	14	21	AA126147	Oestrogen receptor
c 44	12	60.0	20	21	AA166803	Dog genomic marker
c 45	12	60.0	20	22	AA165575	Human focal adhesi

ALIGNMENTS

RESULT 1
AAC65550
ID. AAC65550 standard; DNA; 20 BP.
XX
AC AAC65550;
XX
DT 12-FEB-2001 (first entry)
XX
DE Human focal adhesion kinase antisense sequence #16.
DE
KW Human; focal adhesion kinase; FAK; signal transduction; cancer;
KW embryonic development disorder; angiogenic disorder; wound healing;
KW antisense; phosphothioate; ss.
XX
OS Homo sapiens.
XX
PN US6133031-A.
XX
PD 17-OCT-2000.
XX
PF 19-AUG-1999; 99US-0377310.
XX
PR 19-AUG-1999; 99US-0377310.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Monia BP, Gaarde WA;
XX
DR WPI; 2001-006141/01.
XX
PT New antisense compounds for inhibiting focal adhesion kinase
PT expression, especially useful for inhibiting retinal
PT neovascularization, or for diagnosing and treating e.g. colon cancer -

PS Claim 3; Column 23; 30pp; English.

XX The present invention describes a number of phosphorothioate antisense
CC sequences to the human focal adhesion kinase (FAK) protein. This protein
CC is involved in integrin-mediated signal transduction, and is implicated
CC in cancer, particularly colon, breast and oral tumours, embryonic
CC development disorders, angiogenic disorders and wound healing. The
CC antisense sequences, including the one shown here, can be used in the
CC treatment of all of these.

XX Sequence 20 BP; 5 A; 5 C; 3 G; 7 T; 0 other;

Query Match 100.0%; Score 20; DB 22; Length 20;

Best Local Similarity 100.0%; Pred. No. 0.22; Mismatches 0; Gaps 0;

Qy 1 tttaaccagatggtcattc 20
|||||

Db 1 tttaaccagatggtcattc 20

RESULT 2

AAC65570

ID AAC65570 standard; DNA; 15 BP.

AC AAC65570;

DT 12-FEB-2001 (first entry)

XX Human focal adhesion kinase antisense sequence #36.

XX Human; focal adhesion kinase; FAK; signal transduction; cancer;

KW embryonic development disorder; angiogenic disorder; wound healing;

KX antisense; phosphorothioate; ss.

OS Homo sapiens.

XX US6133031-A.

XX 17-OCT-2000.

PF 19-AUG-1999; 99US-0377310.

PR 19-AUG-1999; 99US-0377310.

XX (ISIS-) ISIS PHARM INC.

PA Monia BP, Gaarde WA;

PI WPI; 2001-006141/01.

XX New antisense compounds for inhibiting focal adhesion kinase

PT expression, especially useful for inhibiting retinal

PT neovascularization, or for diagnosing and treating e.g. colon cancer -

XX Example 2; Column 25; 30pp; English.

PS The present invention describes a number of phosphorothioate antisense
CC sequences to the human focal adhesion kinase (FAK) protein. This protein
CC is involved in integrin-mediated signal transduction, and is implicated
CC in cancer, particularly colon, breast and oral tumours, embryonic
CC development disorders, angiogenic disorders and wound healing. The
CC antisense sequences, including the one shown here, can be used in the
CC treatment of all of these.

XX Sequence 15 BP; 5 A; 4 C; 3 G; 3 T; 0 other;

Query Match

Best Local Similarity 75.0%; Score 15; DB 22; Length 15;

Mismatches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 tcaaccagatggtca 17
|||||

Db 1 tcaaccagatggtca 15

RESULT 3

AAx86411/c

ID AAX86411 standard; DNA; 38 BP.

XX AAX86411;

XX 29-SEP-1999 (first entry)

DE PCR primer PDZK5.5Q used to amplify DNA encoding MMSC1 protein.

XX Human; MMSC1 protein; MMAC1 interacting protein; tumour suppression;

KW MMAC1 pathway; immunogen; cancer; cell neoplastic growth; PCR primer; ss.

XX Synthetic.

OS Homo sapiens.

PN WO9936566-A1.

XX 22-JUL-1999.

PF 19-JAN-1999; 99WO-US00995.

PR 20-JAN-1998; 98US-0071861.

XX (MYRI-) MYRIAD GENETICS INC.

PI Bartel PL, Tavtigian SV;

DR WPI; 1999-458472/38.

PT MMSC1, an MMAC1 (tumour suppressor) interacting protein and related
PT polynucleotides

XX Example 5; Page 50; 107pp; English.

XX PCR primers AAX86368-X86423 were used to amplify DNA encoding a human
CC MMSC1 protein. The PCR templates were derived from tumour cell lines,
CC and the amplicons were tested for mutations. The MMSC1 protein is a
CC MMAC1 interacting protein which is involved in tumour suppression
CC activity in the MMAC1 pathway. MMSC1, antigenic fragments or fusion
CC proteins of these are used as immunogens for antibody production. Primers
CC derived from MMSC1 genomic clones can be used for identification of MMSC1
CC genes and for synthesis by amplification of MMSC1 DNA or RNA. Detecting
CC an alteration in MMSC1 can be used to diagnose cancer. A germline
CC A somatic mutation in an MMSC1 gene is indicative of a predisposition to cancer.
CC A cancerous. Analysis of MMAC1 and MMSC1 (or PDZ domain 6 of MMSC1)
CC binding interactions can be used for detection of alterations in MMAC1
CC associated with cancer. Wild-type MMSC1 or a homologue can be used to
CC supply wild-type MMSC1 gene function (or a substantially similar
CC function) to a cell, which has lost the gene function due to a MMSC1
CC gene mutation. The gene suppresses neoplastic growth of the cell.
CC Transgenic animals having an altered MMSC1 can be used as a model for
CC identifying drug candidates useful in treating cancer.

XX Sequence 38 BP; 11 A; 10 C; 8 G; 9 T; 0 other;

Query Match 72.0%; Score 14.4; DB 20; Length 38;

Best Local Similarity 93.8%; Pred. No. 2e+02; Mismatches 1; Indels 0; Gaps 0;

Qy 3 tcaaccagatggtcat 18

Db 27 TCAATCAGATGTCAT 12

RESULT 4

AAV14039

ID AAA14039 standard; DNA; 20 BP.
 AC AAA14039;
 XX 18-JUL-2000 (first entry)
 XX Human liver glycogen phosphorylase antisense oligo, SEQ ID NO:39.
 DE
 XX Liver glycogen phosphorylase; PYGL gene; human; chromosome 14;
 KW 1,4-alpha-D-glucan:orthophosphate alpha-D-glucosyltransferase; HGLPa;
 KW glycogenolysis; carbohydrate metabolism; blood glucose homeostasis;
 KW expression inhibition; hypoglycemic; type II diabetes;
 KW non insulin-dependent; antisense; phosphorothioate; ss.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH modified_base 1..20
 FT /*tag= a
 FT /note= "Phosphorothioate linkages"
 XX
 XX US6043091-A.
 XX 28-MAR-2000.
 XX 19-JUL-1999; 99US-0357071.
 XX 19-JUL-1999; 99US-0357071.
 XX (ISIS-) ISIS PHARM INC.
 XX Monia BP, Cowser LM;
 XX WPI; 2000-270346/23.
 XX
 XX Antisense compounds particularly oligonucleotides useful for
 PT prophylaxis, diagnosis and treatment of diseases associated with
 PT expression of liver glycogen phosphorylase
 XX
 XX Claim 3; Column 40; 33pp; English.

Sequences AAA14008-A14047 represent phosphorothioate antisense oligonucleotides targeted to the human liver glycogen phosphorylase gene (PYGL gene), which inhibit its expression. The antisense oligonucleotides were designed to target different regions of human liver glycogen phosphorylase RNA, and were analysed for their effect on liver glycogen phosphorylase levels by quantitative real-time PCR. Liver glycogen phosphorylase is one of three glycogen phosphorylase isozymes, which differ in their tissue-specific distribution, immunological properties and electrophoretic mobilities and are encoded by three different genes. Liver glycogen phosphorylase is encoded by the PYGL gene, which is located on chromosome 14. Liver glycogen phosphorylase (also known as 1,4-alpha-D-glucan:orthophosphate alpha-D-glucosyltransferase, and HGLPa in its phosphorylated, active form) catalyses the degradation of stored glycogen in the liver to glucose-1-phosphate via the cleavage of the alpha-1,4-glycosidic bonds. It therefore plays a critical role in carbohydrate metabolism and blood glucose homeostasis. Inhibition of liver glycogen phosphorylase and therefore glycogenolysis may provide a means of reducing blood glucose levels in diabetic patients, particularly those with type II (non insulin-dependent) diabetes. The antisense oligonucleotides of the invention are useful for diagnosis, prevention and treatment of conditions associated with liver glycogen phosphorylase expression, or those which may benefit from inhibition of liver glycogen phosphorylase expression, such as type II diabetes.

XX Sequence 20 BP; 5 A; 5 C; 4 G; 6 T; 0 other;

Query Match 71.0%; Score 14.2; DB 21; Length 20;
 Best Local Similarity 84.2%; Pred. No. 2.3e+02;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 tttaaccagatggtcatt 19
 || ||||| |||||
 Db 1 tttaaccatagggtcatt 19

RESULT 5

AAV51245/C
 ID AAV51245 standard; DNA; 41 BP.
 XX
 AC AAV51245;
 XX 11-JAN-1999 (first entry)
 DT
 DE Maize polymorphic marker S02G2/GS-2 DNA.
 XX
 KW Polymorphic marker; allele-specific; primer; probe; amplification;
 KW hybridisation; plant; hybrid certification; genetic contribution;
 KW progeny; back-cross; hybrid; ancestry; maize; ss.
 XX
 OS Zea mays.
 XX
 XX Key Location/Qualifiers
 FH variation 21
 FT /*tag= a
 FT /replace= "c"
 FT /note= "polymorphism"
 XX
 XX WO9824796-A1.
 XX 11-JUN-1998.
 XX 01-DEC-1997; 97WO-US21782.
 XX 07-MAR-1997; 97US-0813507.
 XX 02-DEC-1996; 96US-0032069.
 XX (AFFY-) AFFYMETRIX INC.
 XX Landry BS, Lemieux B, Murigneux A, Sapolsky RJ;
 XX WPI; 1998-333252/29.

Brassica species allele-specific oligonucleotide probes and primers - useful for plant breeding
 XX Claim 1; Page 49; 65pp; English.
 XX This DNA sequence is a region of a Zea mays genome which contains a polymorphic marker. This sequence can be used in the construction of allele-specific primers and probes for amplification or hybridisation, e.g. to determine common or disparate ancestry between 2 or more plants, to monitor the genetic contribution of an ancestral plant, to trace the progeny of proprietary plants, in certification of a hybrid plant or to identify the progeny of a back-crossed plant with an ancestral plant.
 XX Sequence 41 BP; 8 A; 8 C; 13 G; 12 T; 0 other;

Query Match 69.0%; Score 13.8; DB 19; Length 41;
 Best Local Similarity 88.2%; Pred. No. 4.2e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 caaccagatggtcatt 20
 ||||| |||||
 Db 22 CCACGAGATGTCATC 6

RESULT 6

AAV51246/C
 ID AAV51246 standard; DNA; 41 BP.
 XX
 AC AAV51246;

```

XX 11-JAN-1999 (first entry)
XX Maize polymorphic marker S02G2/G5-2B DNA.
XX
XX Polymorphic marker; allele-specific; primer; probe; amplification;
XX hybridisation; plant; hybrid certification; genetic contribution;
XX progeny; back-cross; hybrid; ancestry; maize; ss.
XX
XX Zea mays.
XX
XX Key Location/Qualifiers
XX variation 21
XX /*tag= a
XX /replace= "c"
XX /note= "polymorphism"
XX
XX WO9824796-A1.
XX
XX 11-JUN-1998.
XX
XX 01-DEC-1997; 97WO-US21782.
XX
XX 07-MAR-1997; 97US-0813507.
XX
XX 02-DEC-1996; 96US-0032069.
XX
XX (AFFY-) AFFYMETRIX INC.
XX
XX Landry BS, Lemieux B, Murigneux A, Sapolsky RJ;
XX
XX WPI; 1998-333252/29.
XX
XX Brassica species allele-specific oligonucleotide probes and primers
XX - useful for plant breeding
XX
XX Claim 1; Page 49; 65pp; English.
XX
XX This DNA sequence is a region of a Zea mays genome which contains a
XX polymorphic marker. This sequence can be used in the construction of
XX allele-specific primers and probes for amplification or hybridisation,
XX e.g. to determine common or disparate ancestry between 2 or more plants,
XX to monitor the genetic contribution of an ancestral plant, to trace the
XX progeny of proprietary plants, in certification of a hybrid plant or to
XX identify the progeny of a back-crossed plant with an ancestral plant.
XX
XX Sequence 41 BP; 9 A; 9 C; 12 G; 11 T; 0 other;
XX
XX
XX Query Match 69.0%; Score 13.8; DB 19; Length 41;
XX Best Local Similarity 88.2%; Pred. NO. 4.2e+02;
XX Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX Qy 4 caaccagatggtcattc 20
XX | | | | | | | | | |
XX Db 22 CCACGAGATGGTCATTC 6
XX
XX
XX RESULT 7
XX AAV47956/c
XX ID AAV47956 standard; DNA; 41 BP.
XX
XX AC AAV47956;
XX
XX DT 14-OCT-1998 (first entry)
XX
XX DE Maize polymorphic site oligonucleotide marker UMC76-G2/G5-2.
XX
XX KW Maize; marker; probe; PCR primer; polymorphism; vegetal sequence;
XX polymorphic site; corn; gramineae species; ss.
XX
XX OS Synthetic.
XX
XX OS Zea sp.
XX
XX PN WO9830717-A2.
XX
XX PD 16-JUL-1998.

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PN WO9830717-A2.
XX
XX PD 16-JUL-1998.
XX
XX PF 02-DEC-1997; 97WO-EP07134.
XX
XX PR 02-DEC-1996; 96US-0032069.
XX
XX PA (BIOC-) BIOCEM SA.
XX
XX PI Murigneux A;
XX
XX DR WPI; 1998-399160/34.
XX
XX PT Vegetal sequences including single nucleotide polymorphism - useful,
XX e.g. to determine polymorphisms in plants, determine strain in plant
XX breeding and to correlate polymorphisms with phenotypic traits
XX
XX Claim 2; Page 15; 32pp; English.
XX
XX The present invention describes a nucleic acid segment comprising at
XX least 10 contiguous nucleotides from a vegetal sequence including a
XX polymorphic site which is a single nucleotide polymorphism (SNP), or the
XX complement of the segment. Also described are: (1) an allele-specific
XX oligonucleotides hybridising to segment, or their complements, and (2) a
XX method of analysing nucleic acids from a subject, by determining if a
XX base is occupying any one (or a set) of polymorphic sites in 261
XX sequences derived from six maize lines (see AAV47701 to AAV47961). The
XX segments are useful in fingerprint analysis in plants to determine which
XX polymorphisms are present, which strain a plant belongs to and to
XX distinguish between strains. The polymorphisms may correlate with
XX phenotypic traits (e.g. plant growth rate or crop yield), and the
XX segments are useful to determine the presence/absence of specific
XX polymorphisms correlating with the existence/absence of particular
XX traits. The segments are also useful in marker assisted back-cross
XX techniques to select plants with a higher percentage of recurrent parent
XX in a back-cross population. Segments incorporate SNPs which occur more
XX frequently than other polymorphism types and are therefore more likely
XX to be located close to genetic loci of interest; different forms of
XX characterised SNPs are also often easier to detect than other
XX polymorphism types.
XX
XX Sequence 41 BP; 8 A; 8 C; 12 G; 12 T; 1 other;
XX
XX
XX Query Match 69.0%; Score 13.8; DB 19; Length 41;
XX Best Local Similarity 88.2%; Pred. No. 4.2e+02;
XX Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX Qy 4 caaccagatggtcattc 20
XX | | | | | | | | | |
XX Db 22 CSACGAGATGGTCATTC 6
XX
XX
XX RESULT 8
XX AAV47957/c
XX ID AAV47957 standard; DNA; 41 BP.
XX
XX AC AAV47957;
XX
XX DT 14-OCT-1998 (first entry)
XX
XX DE Maize polymorphic site oligonucleotide marker UMC76-G2/G5-2B.
XX
XX KW Maize; marker; probe; PCR primer; polymorphism; vegetal sequence;
XX polymorphic site; corn; gramineae species; ss.
XX
XX OS Synthetic.
XX
XX OS Zea sp.
XX
XX PN WO9830717-A2.
XX
XX PD 16-JUL-1998.

```


PI Landry BS, Lemieux B, Murigneux A, Sapolsky RJ;

XX DR WPI; 1998-333252/29.

XX Brassica species allele-specific oligonucleotide probes and primers
PT - useful for plant breeding

XX PS Claim 1; Page 49; 65pp; English.

XX This DNA sequence is a region of a Zea mays genome which contains a
CC polymorphic marker. This sequence can be used in the construction of
CC allele-specific primers and probes for amplification or hybridisation,
CC e.g. to determine common or disparate ancestry between 2 or more plants,
CC to monitor the genetic contribution of an ancestral plant, to trace the
CC progeny of proprietary plants, in certification of a hybrid plant or to
CC identify the progeny of a back-crossed plant with an ancestral plant.

XX Sequence 41 BP; 8 A; 9 C; 11 G; 13 T; 0 other;

Query Match 67.0%; Score 13.4; DB 19; Length 41;

Best Local Similarity 93.3%; Pred. No. 6.8e+02;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 accagatggtcattc 20

II | | | | | | | | | |

Db 40 ACGAGATGTCATTC 26

RESULT 11

AAV47954/c
ID AAV47954 standard; DNA; 41 BP.

XX AC AAV47954;

XX DT 14-OCT-1998 (first entry)

XX DE Maize polymorphic site oligonucleotide marker UMC76-G2/G5-1.

XX KW Maize; marker; probe; PCR primer; polymorphism; vegetal sequence;
KW polymorphic site; corn; gramineae species; ss.

XX OS Synthetic.

XX Zea sp.

XX PN WO9830717-A2.

XX PD 16-JUL-1998.

XX PF 02-DEC-1997; 97WO-EP07134.

XX PR 02-DEC-1996; 96US-0032069.

XX PA (BIOC-) BIOCEM SA.

XX PI Murigneux A;

XX DR WPI; 1998-399160/34.

XX Vegetal sequences including single nucleotide polymorphism - useful,
PT e.g. to determine polymorphisms in plants, determine strain in plant
PT breeding and to correlate polymorphisms with phenotypic traits

XX PS Claim 2; Page 15; 32pp; English.

XX The present invention describes a nucleic acid segment comprising at
CC least 10 contiguous nucleotides from a vegetal sequence including a
CC polymorphic site which is a single nucleotide polymorphism (SNP), or the
CC complement of the segment. Also described are: (1) an allele-specific
CC oligonucleotides hybridising to segment, or their complements, and (2) a
CC method of analysing nucleic acids from a subject, by determining if a
CC base is occupying any one (or a set) of polymorphic sites in 261
CC sequences derived from six maize lines (see AAV47701 to AAV47961). The

CC segments are useful in fingerprint analysis in plants to determine which
CC polymorphisms are present, which strain a plant belongs to and to
CC distinguish between strains. The polymorphisms may correlate with
CC phenotypic traits (e.g. plant growth rate or crop yield), and the
CC segments are useful to determine the presence/absence of specific
CC polymorphisms correlating with the existence/absence of particular
CC traits. The segments are also useful in marker assisted back-cross
CC techniques to select plants with a higher percentage of recurrent parent
CC in a back-cross population. Segments incorporate SNPs which occur more
CC frequently than other polymorphism types and are therefore more likely
CC to be located close to genetic loci of interest; different forms of
CC characterised SNPs are also often easier to detect than other
CC polymorphism types.

XX Sequence 41 BP; 8 A; 8 C; 11 G; 13 T; 1 other;

Query Match 67.0%; Score 13.4; DB 19; Length 41;

Best Local Similarity 93.3%; Pred. No. 6.8e+02;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 accagatggtcattc 20

II | | | | | | | | | |

Db 40 ACGAGATGTCATTC 26

RESULT 12

AAV47955/c
ID AAV47955 standard; DNA; 41 BP.

XX AC AAV47955;

XX DT 14-OCT-1998 (first entry)

XX DE Maize polymorphic site oligonucleotide marker UMC76-G2/G5-1B.

XX KW Maize; marker; probe; PCR primer; polymorphism; vegetal sequence;
KW polymorphic site; corn; gramineae species; ss.

XX OS Synthetic.

XX Zea sp.

XX PN WO9830717-A2.

XX PD 16-JUL-1998.

XX PF 02-DEC-1997; 97WO-EP07134.

XX PR 02-DEC-1996; 96US-0032069.

XX PA (BIOC-) BIOCEM SA.

XX PI Murigneux A;

XX DR WPI; 1998-399160/34.

XX Vegetal sequences including single nucleotide polymorphism - useful,
PT e.g. to determine polymorphisms in plants, determine strain in plant
PT breeding and to correlate polymorphisms with phenotypic traits

XX PS Claim 2; Page 15; 32pp; English.

XX The present invention describes a nucleic acid segment comprising at
CC least 10 contiguous nucleotides from a vegetal sequence including a
CC polymorphic site which is a single nucleotide polymorphism (SNP), or the
CC complement of the segment. Also described are: (1) an allele-specific
CC oligonucleotides hybridising to segment, or their complements, and (2) a
CC method of analysing nucleic acids from a subject, by determining if a
CC base is occupying any one (or a set) of polymorphic sites in 261
CC sequences derived from six maize lines (see AAV47701 to AAV47961). The
CC segments are useful in fingerprint analysis in plants to determine which
CC polymorphisms are present, which strain a plant belongs to and to
CC distinguish between strains. The polymorphisms may correlate with

CC phenotypic traits (e.g. plant growth rate or crop yield), and the
 CC segments are useful to determine the presence/absence of specific
 CC polymorphisms correlating with the existence/absence of particular
 CC traits. The segments are also useful in marker assisted back-cross
 CC techniques to select plants with a higher percentage of recurrent parent
 CC in a back-cross population. Segments incorporate SNPs which occur more
 CC frequently than other polymorphism types and are therefore more likely
 CC to be located close to genetic loci of interest; different forms of
 CC characterised SNPs are also often easier to detect than other
 CC polymorphism types.

XX Sequence 41 BP; 8 A; 9 C; 10 G; 13 T; 1 other;
 SQ

Query Match 67.0%; Score 13.4; DB 19; Length 41;

Best Local Similarity 93.3%; Pred. No. 6.8e+02;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 accagatggtcattc 20

|||||||

Db 40 ACGAGATGGTCAATC 26

RESULT 13

AAZ55314/C

ID AAZ55314 standard; DNA; 33 BP.

XX

AC AAZ55314;

XX

DT 21-MAR-2000 (first entry)

XX

DE Neisseria species ORF cloning PCR primer #699.

XX

KW Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;

KW antigenic; diagnosis; immunogenic; infection; meningitis; septicaemia;

KW antibacterial; gene therapy; PCR primer; ss.

XX

OS Synthetic.

OS Neisseria sp.

PN WO9957280-A2.

XX

PD 11-NOV-1999.

XX

PF 30-APR-1999; 99WO-US09346.

XX

PR 01-MAY-1998; 98US-0083758.

PR 31-JUL-1998; 98US-0094869.

PR 02-SEP-1998; 98US-0098994.

PR 02-SEP-1998; 98US-0099062.

PR 09-OCT-1998; 98US-0103749.

PR 09-OCT-1998; 98US-0103794.

PR 09-OCT-1998; 98US-0103796.

PR 25-FEB-1999; 99US-0121528.

XX

PA (CHIR) CHIRON CORP.

PA (GENO-) INST GENOMIC RES.

XX

PI Fraser C, Galeotti C, Grandi G, Hickey E, Masignani V, Mora M;

PI Petersen J, Pizza M, Rappuoli R, Ratti G, Scalato E, Scarselli M;

PI Tettelin H, Venter JC;

XX

DR WPI; 2000-062150/05.

XX

XX Novel Neisserial polypeptides predicted to be useful antigens for

PT vaccines and diagnostics -

PT

XX Example 16; Page 160; 1453pp; English.

XX

CC AAZ53015 to AAZ54536, AAZ54577 to AAZ54615, and AAY74253 to AAY75941

CC represent novel Neisseria meningitidis and N. gonorrhoeae polynucleotides

CC and polypeptides. AAZ54537 to AAZ54576 and AAZ54616 to AAZ54573 represent

CC PCR primers used in the exemplification of the present invention. The

CC polypeptides, the polynucleotides, antibodies and compositions of
 CC the invention can be used as vaccines, as diagnostic reagents, and as
 CC immunogenic compositions. The polypeptides can be used in the
 CC manufacture of medicaments for treating or preventing infection due to
 CC Neisserial bacteria (e.g. meningitis and septicaemia), to detect the
 CC presence of Neisseria bacteria, or to raise antibodies. They may also
 CC be used to screen for agonists or antagonists, which may themselves
 CC have use as antibacterial agents. The polynucleotides of the invention
 CC may also be used in gene therapy protocols.

XX

SQ Sequence 33 BP; 11 A; 10 C; 4 G; 8 T; 0 other;

Query Match 66.0%; Score 13.2; DB 21; Length 33;

Best Local Similarity 83.3%; Pred. No. 8.3e+02;

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 tttaacaccagatggtcat 18

|||||

Db 30 TTTGAAATAGATGTCAT 13

RESULT 14

AAZ52031

ID AAZ52031 standard; DNA; 50 BP.

XX

AC AAZ52031;

XX

DT 18-JUN-1999 (first entry)

XX

DE Synthetic plasmid synlux4 construction oligonucleotide F11.

XX

KW DNA plasmid; lux A; lux B; Vibrio fischeri; luciferase; promoter;

KW ttr9 kanamycin/neomycin phosphotransferase; DNA synthesis;

KW kanamycin/neomycin phosphotransferase; DNA synthesis; ss.

XX

OS Synthetic.

PN WO9914318-A1.

XX

PD 25-MAR-1999.

XX

PF 16-SEP-1998; 98WO-US19312.

XX

PR 16-SEP-1997; 97US-0059017.

XX

PA (TEXA) UNIV TEXAS SYSTEM.

XX

PI Evans GA;

XX

DR WPI; 1999-244029/20.

XX

PT Synthesis of replication competent double-stranded polynucleotides

XX

PS Example 4; Fig 5A; 135pp; English.

XX

CC AAZ52021-212 represent oligonucleotide primers that were used to
 CC construct a synthetic DNA plasmid sequence synlux4, to demonstrate the
 CC method of the invention. Within the synlux4 sequence are included the
 CC sequences of lux A, lux B, the A and B components of the Vibrio fischeri
 CC luciferase sequence, positions of pUC19 including the origin of
 CC replication and replication stability sequences, and the promoter and
 CC coding sequence for ttr9 kanamycin/neomycin phosphotransferase. The
 CC specification describes a method for the synthesis of replication
 CC competent double-stranded polynucleotides. The method comprises
 CC generating a first set of oligonucleotides corresponding to the plus
 CC strand and a second set corresponding to the minus strand and
 CC annealing. The method can be used for preparing polynucleotides
 CC encoding sequences involved in a biochemical pathway. In particular,
 CC they can be used to produce polynucleotides encoding enzymes,
 CC e.g. hexokinase, phosphohexose isomerase, phosphofructokinase-1,
 CC aldolase, triose-phosphate isomerase, glyceraldehyde-3-phosphate
 CC dehydrogenase, phosphoglycerate kinase, phosphoglycerate mutase,

CC enolase or pyruvate kinase. They can also be used for the preparation
XX of viral particles, artificial genomes and artificial genetic systems.

SQ Sequence 50 BP; 21 A; 9 C; 8 G; 12 T; 0 other;
Search completed: October 2, 2001, 16:18:45
Job time: 15489 sec

Query Match 66.0%; Score 13.2; DB 20; Length 50;
Best Local Similarity 83.3%; Pred. NO. 8.9e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 tttaaccagatgggtcat 18
||||| ||||| |||
Db 14 ttctaccagatgataat 31

RESULT 15

AAV28114
ID AAV28114 standard; DNA; 25 BP.

XX AC AAV28114;

XX DT 26-OCT-1998 (first entry)

XX DE Rat 5-oxoprolinase PCR primer.

XX KW 5-oxoprolinase; rat; glutathione; 5-oxoprolinuria; gene therapy;

XX OS diagnosis; PCR; primer; ss.

XX OS Synthetic.

XX OS Rattus sp.

XX PN WO9825945-A1.

XX PD 18-JUN-1998.

XX PF 04-DEC-1997; 97WO-US22851.

XX PR 09-DEC-1996; 96US-0762428.

XX PA (CORR) CORNELL RES FOUND INC.

XX PI Breslow E, Meister A, Ye G;

XX PS WPI; 1998-348440/30.
Mammalian 5-oxoprolinase - useful for developing products for
treating 5-oxoprolinuria

XX PS Disclosure; Page 32; 66pp; English.

XX This PCR primer was used in the amplification of 5-oxoprolinase
CC cDNA (see also AAV28111-12) from rat kidney cDNA. The primer
CC incorporates an NdeI site at the start codon of the 5-oxoprolinase.
CC cDNA. The PCR product was used in the construction of expression
CC plasmids for 5-oxoprolinase. Mammalian 5-oxoprolinase (m5OP)
CC catalyzes the ATP dependent cleavage of 5-oxoprolinase to L-glutamate
CC in the metabolism of glutathione. Deficiency of the enzyme is
CC associated with 5-oxoprolinuria. The invention is directed toward
CC isolated nucleic acid molecules encoding m5OP. Expression vectors
CC and host cells are provided, as well as methods of increasing (by
CC gene therapy) or decreasing (e.g. using antisense or ribozyme
CC molecules) the expression of m5OP in host cells.

XX Sequence 25 BP; 6 A; 9 C; 5 G; 5 T; 0 other;

Query Match 64.0%; Score 12.8; DB 19; Length 25;

Best Local Similarity 87.5%; Pred. NO. 1.3e+03;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 tttaaccagatgggtca 17

||||| ||||| |||

Db 8 tttaaccataggcca 23

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: October 2, 2001, 16:03:51 ; Search time 417.38 Seconds
(without alignments)
9.071 Million cell updates/sec

Title: US-09-757-100B-17
Perfect score: 20
Sequence: 1 attctcgtcgtgtgga 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 324599 seqs, 9465562 residues

Total number of hits satisfying chosen parameters: 460742

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA.*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq.*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	3	US-09-377-310-17
c 2	15.2	76.0	40	1	US-08-040-548-52
c 3	15.2	76.0	40	1	US-08-466-344-52
4	15	75.0	15	3	US-09-377-310-37
5	14.8	74.0	32	4	US-08-686-968C-20
c 6	14.2	71.0	20	2	US-08-628-422-16
c 7	13.4	67.0	18	2	US-08-313-185-16
c 8	13.4	67.0	18	3	US-09-082-614A-16
c 9	13.4	67.0	26	2	US-08-861-450-2
10	12.8	64.0	21	1	US-08-647-351B-3
c 11	12.6	63.0	30	3	US-09-392-580-43
c 12	12.6	63.0	30	1	US-08-295-670-3
13	12.5	63.0	30	1	US-08-633-485-3
14	12.2	61.0	20	1	US-08-202-042-4
15	12.2	61.0	21	4	US-08-430-225A-13
16	12.2	61.0	24	1	US-07-923-724-12
17	12.2	61.0	24	2	US-08-609-426A-12
c 18	12.2	61.0	29	1	US-07-642-734C-19
c 19	12.2	61.0	29	3	US-08-439-009A-19
20	12.2	61.0	31	3	US-09-123-764-5
c 21	12.2	61.0	31	5	PCT-US94-07091-1
22	12.2	61.0	38	3	US-08-938-830-19
23	12.2	61.0	38	3	US-09-020-222-19
24	12.2	61.0	39	4	US-08-993-674A-66
c 25	12.2	61.0	42	2	US-08-124-981A-18
c 26	12.2	61.0	42	3	US-09-037-190-16
c 27	12.2	61.0	42	3	US-09-037-192-16

c 28	12.2	61.0	42	3	US-09-037-143-16
c 29	12.2	61.0	42	4	US-09-049-691-16
c 30	12.2	61.0	42	4	US-08-260-174-16
c 31	12.2	61.0	49	4	US-08-993-674A-67
c 32	12	60.0	27	2	US-08-859-998-1095
c 33	12	60.0	28	1	US-08-558-719-2
c 34	12	60.0	28	2	US-08-558-651-2
c 35	12	60.0	31	1	US-07-866-560-2
c 36	12	60.0	31	1	US-07-866-979-2
c 37	12	60.0	31	1	US-08-077-673-2
c 38	12	60.0	31	1	US-08-478-992-2
c 39	12	60.0	31	3	US-09-105-298-2
c 40	12	60.0	33	4	US-09-232-468A-38
c 41	12	60.0	45	1	US-08-067-160-19
c 42	12	60.0	45	2	US-08-717-394-19
c 43	12	60.0	45	2	US-08-487-110-19
c 44	12	60.0	45	3	US-09-028-648A-19
c 45	12	60.0	45	3	US-09-028-587-19

ALIGNMENTS

RESULT 1
US-09-377-310-17
; Sequence 17, Application US/09377310B
; Patent No. 6133031
; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P.
; APPLICANT: Gaarde, William A.
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
; TITLE OF INVENTION: Expression
; FILE REFERENCE: ISPH-0389
; CURRENT APPLICATION NUMBER: US/09/377,310B
; CURRENT FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
US-09-377-310-17

Query Match 100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.39;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 attctcgtcgtgtgga 20
Db 1 attctcgtcgtgtgga 20

RESULT 2
US-08-040-548-52/c
; Sequence 52, Application US/08040548
; Patent No. 5763209
; GENERAL INFORMATION:
; APPLICANT: Sukhatme, Vikas P.
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO THE
; TITLE OF INVENTION: FUNCTIONAL DOMAINS OF DNA BINDING PROTEINS
; NUMBER OF SEQUENCES: 67
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: 321 No. 5763209th Clark Street, Suite 800
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60610
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/040,548
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Coughlin, Daniel F.
REGISTRATION NUMBER: 36,111
REFERENCE/DOCKET NUMBER: arcd067
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 744-0090
TELEFAX: (312) 245-4961
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-040-548-52

Query Match 76.0%; Score 15.2; DB 1; Length 40;
Best Local Similarity 85.0%; Pred. No. 72;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 attctcgtcgtcgtggtgaa 20
||||||| ||||| |||||
Db 21 ATTCTCGTGTCTGCCGAA 2

RESULT 3
US-08-466-344-52/c
Sequence 52, Application US/08466344
Patent No. 5773583
GENERAL INFORMATION:
APPLICANT: Sukhatme, Vikas P.
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO THE
TITLE OF INVENTION: FUNCTIONAL DOMAINS OF DNA BINDING PROTEINS
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: 321 No. 5773583th Clark Street, Suite 800
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60610

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,344
FILING DATE: 06-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/040,548
FILING DATE: 31-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Coughlin, Daniel F.
REGISTRATION NUMBER: 36,111
REFERENCE/DOCKET NUMBER: arcd067
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 744-0090
TELEFAX: (312) 245-4961
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-466-344-52

Query Match 76.0%; Score 15.2; DB 1; Length 40;
Best Local Similarity 85.0%; Pred. No. 72;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 attctcgtcgtcgtggtgaa 20
||||||| ||||| |||||
Db 21 ATTCTCGTGTCTGCCGAA 2

RESULT 4
US-09-377-310-37
Sequence 37, Application US/09377310B
Patent No. 6133031
GENERAL INFORMATION:
APPLICANT: Monia, Brett P.
APPLICANT: Gaarde, William A.
TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
TITLE OF INVENTION: Expression
FILE REFERENCE: ISPH-0389
CURRENT APPLICATION NUMBER: US/09/377,310B
CURRENT FILING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 37
LENGTH: 15
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: antisense sequence
US-09-377-310-37

Query Match 75.0%; Score 15; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 tctcgtcgtcgtggtg 17
||||||| ||||| |||||
Db 1 tctcgtcgtcgtggtg 15

RESULT 5
US-08-686-968C-20
Sequence 20, Application US/08686968C
Patent No. 6221361
GENERAL INFORMATION:
APPLICANT: Cochran, Mark D.
APPLICANT: Junker, David E.
TITLE OF INVENTION: Recombinant Swinepox Virus
FILE REFERENCE: 39119-H/JML
CURRENT APPLICATION NUMBER: US/08/686,968C
CURRENT FILING DATE: 1996-07-25
NUMBER OF SEQ ID NOS: 231
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 20
LENGTH: 32
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: primer
US-08-686-968C-20

Query Match 74.0%; Score 14.8; DB 4; Length 32;
Best Local Similarity 88.9%; Pred. No. 1.le+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 attctcgtcgtcgtggtg 18

Db 15 attctgctgagtgtg 32
||||| ||||| |||||
RESULT 6
US-08-628-422-16/c
; Sequence 16, Application US/08628422
; Patent No. 5837854
; GENERAL INFORMATION:
; APPLICANT: Mulder, Carel
; TITLE OF INVENTION: OLIGONUCLEOTIDES WITH ANTI-EPSTEIN-BARR
; TITLE OF INVENTION: VIRUS ACTIVITY
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/628,422
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Fasse, J. Peter
; REGISTRATION NUMBER: 32,983
; REFERENCE/DOCKET NUMBER: 04020/094001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-628-422-16
Query Match 71.0%; Score 14.2; DB 2; Length 20;
Best Local Similarity 84.2%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2 ttctcgtcgtcgtgtaa 20
||| ||||| ||||| |||||
Db 20 TTGCTCGAGCTGGAGAA 2
RESULT 7
US-08-313-185-16/c
; Sequence 16, Application US/08313185
; Patent No. 5851763
; GENERAL INFORMATION:
; APPLICANT: Heym, Beate
; APPLICANT: Cole, Stewart
; APPLICANT: Young, Douglas
; APPLICANT: Zhang, Ying
; APPLICANT: Honore, Nadine
; APPLICANT: Telenti, Amalio
; APPLICANT: Bodmer, Thomas
; TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
; TITLE OF INVENTION: In Mycobacterium tuberculosis
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &

; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/313,185
; FILING DATE: 12-OCT-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 02356.0068-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-313-185-16
Query Match 67.0%; Score 13.4; DB 2; Length 18;
Best Local Similarity 93.3%; Pred. No. 4.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 5 ctgcgtcgtggtgga 19
||||| ||||| |||||
Db 16 CTCGCTGGGGTGA 2
RESULT 8
US-09-082-614A-16/c
; Sequence 16, Application US/09082614A
; Patent No. 6124098
; GENERAL INFORMATION:
; APPLICANT: Heym, Beate
; APPLICANT: Cole, Stewart
; APPLICANT: Young, Douglas
; APPLICANT: Zhang, Ying
; APPLICANT: Honore, Nadine
; APPLICANT: Telenti, Amalio
; APPLICANT: Bodmer, Thomas
; TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
; TITLE OF INVENTION: In Mycobacterium tuberculosis
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/082,614A
; FILING DATE:
; CLASSIFICATION:

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/313,185
; FILING DATE: 12-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 02356-0068-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-09-082-614A-16

Query Match 67.0%; Score 13.4; DB 3; Length 18;
Best Local Similarity 93.3%; Pred. No. 4.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 ctgcgtgctggtgga 19
DB 16 CTCGCTCGGGTGA 2

RESULT 9
US-08-861-450-2/c
; Sequence 2, Application US/08861450
; Patent No. 5908764
; GENERAL INFORMATION:
; APPLICANT: Br nker, Peter
; APPLICANT: Minas, Wolfgang
; APPLICANT: Kallio, Pauli
; APPLICANT: Bailey, James E.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; TITLE OF INVENTION: INCREASING PRODUCTION OF ERYTHROMYCIN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds, LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSEQ for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/861,450
; FILING DATE: 22-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Abrams, Samuel B
; REGISTRATION NUMBER: 30,605
; REFERENCE/DOCKET NUMBER: 9092-0004-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
```

```
; TOPOLOGY: linear
; US-08-861-450-2

Query Match 67.0%; Score 13.4; DB 2; Length 26;
Best Local Similarity 93.3%; Pred. No. 4.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 tcgcgtgctggtgga 20
DB 26 TAGCTGCTGGTGAA 12

RESULT 10
US-08-647-351B-3
; Sequence 3, Application US/08647351B
; Patent No. 5770368
; GENERAL INFORMATION:
; APPLICANT: De Leon, Ricardo
; APPLICANT: Rochelle, Paul
; TITLE OF INVENTION: Cryptosporidium Detection Method
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheldon & Mak
; STREET: 225 S. Lake Avenue, 9th Floor
; CITY: Pasadena
; STATE: California
; ZIP: 91101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows version 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/647,351B
; FILING DATE: May 9, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Farah, David A.
; REGISTRATION NUMBER: 38,134
; REFERENCE/DOCKET NUMBER: 11364
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (626) 796-4000
; TELEFAX: (626) 795-6321
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid
; DESCRIPTION: primer sequence
; US-08-647-351B-3

Query Match 64.0%; Score 12.8; DB 1; Length 21;
Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 ctgcgtgctggtgga 20
DB 4 CTTGCTGCTGGTGAA 19

RESULT 11
US-09-392-580-43/c
; Sequence 43, Application US/09392580
; Patent No. 6087173
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Elizabeth J. Ackermann
; APPLICANT: Lex M. Cowsert
; TITLE OF INVENTION: ANTISENSE MODULATION OF X-LINKED INHIBITOR OF APOPTOSIS EXPRES
```

FILE REFERENCE: RTS-0072
CURRENT APPLICATION NUMBER: US/09/392,580
CURRENT FILING DATE: 1999-09-09
NUMBER OF SEQ ID NOS: 47
SEQ ID NO 43
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-09-392-580-43

Query Match 63.0%; Score 12.6; DB 3; Length 20;
Best Local Similarity 78.9%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 attctcgtcgtcgtgga 19
Db 19 ATTGTTCCATGCTGTTGGA 1

RESULT 12
US-08-295-670-3
Sequence 3, Application US/08295670
Patent No. 5547864
GENERAL INFORMATION:
APPLICANT: KAWASAKI, HISASHI
APPLICANT: TSUCHIYA, MAKOTO
APPLICANT: MIWA, KIYOSHI
APPLICANT: KAWAHARA, YOSHIO
TITLE OF INVENTION: THE NOVEL CELL SURFACE PROTEIN
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/295,670
FILING DATE: 08-SEP-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP94/00039
FILING DATE: 13-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-4069
FILING DATE: 13-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5547864man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-697-0 PCT
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
US-08-295-670-3

Query Match 63.0%; Score 12.6; DB 1; Length 30;
Best Local Similarity 78.9%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 ttctcgtcgtcgtgga 20
Db 1 TTCATCGCTGCTGCGCA 19

RESULT 13
US-08-633-485-3
Sequence 3, Application US/08633485
Patent No. 5681717
GENERAL INFORMATION:
APPLICANT: KAWASAKI, HISASHI
APPLICANT: TSUCHIYA, MAKOTO
APPLICANT: MIWA, KIYOSHI
APPLICANT: KAWAHARA, YOSHIO
TITLE OF INVENTION: THE NOVEL CELL SURFACE PROTEIN
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/633,485
FILING DATE: 17-APR-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/295,670
FILING DATE: 08-SEP-1994
APPLICATION NUMBER: PCT/JP94/00039
FILING DATE: 13-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-4069
FILING DATE: 13-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5681717man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-697-0 PCT
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
US-08-633-485-3

Query Match 63.0%; Score 12.6; DB 1; Length 30;
Best Local Similarity 78.9%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 ttctcgtcgtcgtgga 20
Db 1 TTCATCGCTGCTGCGCA 19

RESULT 14
US-08-202-042-4
; Sequence 4, Application US/08202042
; Patent No. 5686072
; GENERAL INFORMATION:
; APPLICANT: Jonathan W. Uhr
; APPLICANT: Ellen S. Vitetta
; TITLE OF INVENTION: EPTOPO-SPECIFIC MONOCLONAL
; TITLE OF INVENTION: ANTIBODIES AND IMMUNOTOXINS
; TITLE OF INVENTION: AND USES THEREOF
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/202,042
; FILING DATE: Submitted herewith
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: David L. Parker
; REGISTRATION NUMBER: 32,165
; REFERENCE/DOCKET NUMBER: UTSD:379/PAR
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 320-7200
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: oligonucleotide
US-08-202-042-4

Query Match 61.0%; Score 12.2; DB 1; Length 20;
Best Local Similarity 82.4%; Pred. NO. 1.7e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 attctcgtcgtcgtg 17
||| ||||| |||||
Db 4 ATTCTCGCTCGTGTG 20

RESULT 15
US-08-430-225A-13
; Sequence 13, Application US/08430225A
; Patent No. 6204000
; GENERAL INFORMATION:
; APPLICANT: Dong, Jin-Tang; Barrett,
; APPLICANT: J. Carl; Patricia W.; Isaacs, John T.
; TITLE OF INVENTION: DIAGNOSTIC METHODS AND
; TITLE OF INVENTION: GENE THERAPY USING REAGENTS DERIVED FROM THE
; TITLE OF INVENTION: HUMAN METASTASIS SUPPRESSOR GENE KAI1
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK

; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/430,225A
; FILING DATE: 28-APR-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: RICHARD W. BORK
; REGISTRATION NUMBER: 36,459
; REFERENCE/DOCKET NUMBER: 2026-4172
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; TELEX: 421792
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-430-225A-13

Query Match 61.0%; Score 12.2; DB 4; Length 21;
Best Local Similarity 82.4%; Pred. NO. 1.7e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 attctcgtcgtcgtg 17
||| ||||| ||||| ||
Db 1 AGTCTCGCTCGTGTG 17

Search completed: October 2, 2001, 16:03:52
Job time: 14596 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 2, 2001, 16:18:44 ; Search time 876.95 Seconds
(without alignments)
14.320 Million cell updates/sec

Title: US-09-757-100B-17

Perfect score: 20

Sequence: 1 attctcgtctgtgtgaa 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 730101 seqs, 313950809 residues

Total number of hits satisfying chosen parameters: 854978

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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22: /SID88/gcgdata/geneseq/geneseq/NA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	22	AAC65549 Human focal adhesi
2	15	75.0	35	22	AAC65569 Human focal adhesi
3	14.8	74.0	32	19	AAV26137 IBRV gi gene PCR p
4	14.8	74.0	35	21	AAV70370 3' oligonucleotide
5	14.2	71.0	20	18	AAAT92645 BZLF1 gene specifi
6	14	70.0	18	14	AAQ61472 Primer pair #6 Oli
7	14	70.0	18	14	AAV58527 PCR primer used to
8	13.6	68.0	32	15	AAQ88809 BoPCar I, bovine p
9	13.4	67.0	20	20	AAV96509 PCR primer used to
10	13.4	67.0	26	20	AAV96509 PmerR promoter amp
11	13.2	66.0	20	19	AAV96509 Human biallelic po

C 12	13	65.0	23	21	AAC87185 Rice mutant BPSPS
C 13	13	65.0	23	21	AAC88395 Primer Universal r
C 14	13	65.0	23	21	AAC89319 Primer universal r
C 15	12.8	64.0	19	21	AAA82953 cdk6 ribozyme bind
C 16	12.8	64.0	21	18	AAAT89992 Cryptosporidium he
C 17	12.6	63.0	20	20	AAV97166 Primer used to amp
C 18	12.6	63.0	20	21	AAA64943 Antisense oligonuc
C 19	12.6	63.0	30	15	AAV70365 B.lactofermentum c
C 20	12.4	62.0	18	14	AAQ37914 Beta-casein sequen
C 21	12.4	62.0	18	17	AAV27829 Primer #1 for mali
C 22	12.4	62.0	21	21	AAA48928 Reverse primer PB.
C 23	12.4	62.0	29	21	AAV05016 Hammerhead ribozym
C 24	12.4	62.0	31	20	AAV02733 Eubacterial 16S rR
C 25	12.4	62.0	31	21	AAV54559 Primer O265 used t
C 26	12.4	62.0	38	21	AAC69811 E. coli O356 SELEX
C 27	12.2	61.0	20	13	AAV93237 Antisense oligonuc
C 28	12.2	61.0	20	20	AAV04613 PCR primer used to
C 29	12.2	61.0	21	17	AAV40022 Primer for human K
C 30	12.2	61.0	21	19	AAV57633 Exon 1 of an ENAC
C 31	12.2	61.0	24	15	AAV58130 cbh1-Phytase prime
C 32	12.2	61.0	29	14	AAV46797 pAeryAKS2 primer
C 33	12.2	61.0	30	20	AAV16994 A. thaliana endo-1
C 34	12.2	61.0	31	16	AAV76298 Staphylococcus aur
C 35	12.2	61.0	31	18	AAV62574 Granule bound star
C 36	12.2	61.0	31	21	AAV79051 Human genomic DNA
C 37	12.2	61.0	37	9	AAV81428 Sequence of synthe
C 38	12.2	61.0	38	19	AAV57997 Murine PSTPIP PCR
C 39	12.2	61.0	38	21	AAV64251 PCR primer for PTP
C 40	12.2	61.0	38	21	AAV07288 PCR primer for PS
C 41	12.2	61.0	41	21	AAV73359 Single base extens
C 42	12.2	61.0	42	16	AAV86682 NF-AT transcrip tio
C 43	12.2	61.0	42	21	AAV00913 PCR Primer KXF to
C 44	12.2	61.0	42	21	AAV29268 Human nuclear fact
C 45	12.2	61.0	42	22	AAV31700 Human NF-AT polynu

ALIGNMENTS

RESULT 1
AAC65549
ID AAC65549 standard; DNA; 20 BP.
XX
AC AAC65549;
XX
DT 12-FEB-2001 (first entry)
XX
DE Human focal adhesion kinase antisense sequence #15.
XX
KW Human; focal adhesion kinase; FAK; signal transduction; cancer;
KW embryonic development disorder; angiogenic disorder; wound healing;
KW antisense; phosphorothioate; ss.
XX
OS Homo sapiens.
XX
PN US6133031-A.
XX
PD 17-OCT-2000.
XX
PF 19-AUG-1999; 99US-0377310.
XX
PR 19-AUG-1999; 99US-0377310.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Monia BP, Gaarde WA;
XX
DR WPI; 2001-006141/01.
XX
PT New antisense compounds for inhibiting focal adhesion kinase
PT expression, especially useful for inhibiting retinal
PT neovascularization, or for diagnosing and treating e.g. colon cancer -
XX

PS Example 2; Column 23; 30pp; English.

CC The present invention describes a number of phosphorothioate antisense
CC sequences to the human focal adhesion kinase (FAK) protein. This protein
CC is involved in integrin-mediated signal transduction, and is implicated
CC in cancer, particularly colon, breast and oral tumours, embryonic
CC development disorders, angiogenic disorders and wound healing. The
CC antisense sequences, including the one shown here, can be used in the
CC treatment of all of these.

XX Sequence 20 BP; 3 A; 5 C; 6 G; 6 T; 0 other;

Query Match 100.0%; Score 20; DB 22; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.4;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 attctcgtcgtggtgaa 20

|||||

Db 1 attctcgtcgtggtgaa 20

RESULT 2

AAC65569

ID AAC65569 standard; DNA; 15 BP.

AC AAC65569;

DT 12-FEB-2001 (first entry)

XX Human focal adhesion kinase antisense sequence #35.

XX Human; focal adhesion kinase; FAK; signal transduction; cancer;

KW embryonic development disorder; angiogenic disorder; wound healing;

KX antisense; phosphorothioate; ss.

OS Homo sapiens.

PN US6133031-A.

PD 17-OCT-2000.

XX 19-AUG-1999; 99US-0377310.

XX 19-AUG-1999; 99US-0377310.

XX (ISIS-) ISIS PHARM INC.

PI Monla BP, Gaarde WA;

XX WPI; 2001-006141/01.

XX New antisense compounds for inhibiting focal adhesion kinase

PT expression, especially useful for inhibiting retinal

PT neovascularization, or for diagnosing and treating e.g. colon cancer -

XX Example 2; Column 25; 30pp; English.

XX The present invention describes a number of phosphorothioate antisense
CC sequences to the human focal adhesion kinase (FAK) protein. This protein
CC is involved in integrin-mediated signal transduction, and is implicated
CC in cancer, particularly colon, breast and oral tumours, embryonic
CC development disorders, angiogenic disorders and wound healing. The
CC antisense sequences, including the one shown here, can be used in the
CC treatment of all of these.

XX Sequence 15 BP; 0 A; 5 C; 5 G; 5 T; 0 other;

Query Match

Best Local Similarity 75.0%; Score 15; DB 22; Length 15;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 tctcgtcgtcgtggtg 17

|||||

Db 1 tctcgtcgtcgtggtg 15

RESULT 3

AAV26137

ID AAV26137 standard; DNA; 32 BP.

XX AC AAV26137;

XX DT 24-JUL-1998 (first entry)

XX IBRV gI gene PCR primer SEQ ID NO:20 from WO9804684 Example 41.

XX Swinepox virus; SPV; recombinant; vaccine; immunisation; diagnosis;

KW pseudorabies virus; feline immunodeficiency virus; FIV; heartworm;

KW Dirofilaria immitis; PCR primer; ss.

XX OS Synthetic.

XX WO9804684-A1.

XX PD 05-FEB-1998.

XX PF 25-JUL-1997; 97WO-US12212.

XX PR 25-JUL-1996; 96US-0686968.

XX PA (SYTR) SYNTRO CORP.

XX PI Cochran MD, Junker DE;

XX DR WPI; 1998-130677/12.

XX PT Recombinant swine pox virus - useful in vaccine for immunising

XX animal against swine pox virus

XX Example 41; Page 180; 473pp; English.

XX The present sequence represents a PCR primer used in an example from the
CC present invention. The present invention specifically describes
CC recombinant swinepox virus (SPV) comprising a foreign DNA (I) inserted
CC into a SPV genome which is capable of being expressed in a host cell
CC into which the virus is introduced, where (I) is inserted into: (a) an
CC EcoRI site within a region corresponding to a 3.2 kb subfragment of the
CC HindIII K fragment which contains both a HindIII and an EcoRI site, of
CC the SPV genome, and optionally (b) an AccI site within a region
CC corresponding to a 3.6 kb HindIII to BglII subfragment of the HindIII M
CC fragment. The recombinant SPV can be used in a vaccine for immunising an
CC animal against SPV. The invention also provides a method for testing a
CC swine to determine whether the swine has been vaccinated with a
CC vaccine, particularly containing S-SPV-008, or is infected with a
CC naturally occurring wild-type pseudorabies virus. Also (I) inserted into
CC recombinant SPV can be used in a diagnostic assay, e.g. Feline
CC immunodeficiency virus (FIV) env and gag genes and Dirofilaria immitis
CC p39 and 22kd are useful to detect feline immunodeficiency caused by FIV
CC and to detect heartworm caused by D. immitis respectively.

XX Sequence 32 BP; 4 A; 7 C; 10 G; 11 T; 0 other;

Query Match

Best Local Similarity 74.0%; Score 14.8; DB 19; Length 32;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 attctcgtcgtcgtggtg 18

|||||

Db 15 attctcgtcgtggtg 32

RESULT 4

AAA70370

ID AAA70370 standard; DNA; 35 BP.
 AC AAA70370;
 XX
 DT 02-FEB-2001 (first entry)
 DE
 DE 3' oligonucleotide # 1 used for cloning human placental bikunin cDNA.
 XX
 XX Mucociliary dysfunction; mucus; sputum; human;
 KW chronic obstructive lung disease; chronic bronchitis; CB; Bronchiectasis;
 KW BE; asthma; cystic fibrosis; CF; bacterial infection; placental bikunin;
 KW Kunitz-type serine protease inhibitor; chronic sinusitis; glue ear; ss.
 XX
 OS Homo sapiens.
 XX
 XX WO200037099-A2.
 PN
 XX 29-JUN-2000.
 PD
 XX 22-DEC-1999; 99WO-GB04381.
 XX
 XX 22-DEC-1998; 98US-0218913.
 PR
 PR 17-NOV-1999; 99US-0441966.
 XX
 PA (FARB) BAYER AG.
 XX
 XX Hall R, Poll CT, Newton BB, Taylor WJA;
 PI
 XX WPI: 2000-452127/39.
 DR
 XX Stimulating mucociliary clearance rate of mucus and sputum in lung
 PT always for treating lung diseases such as cystic fibrosis and
 PT bronchitis involves administering a Kunitz-type serine protease
 PT inhibitor
 XX
 XX Example 6; Page 52; 173pp; English.
 PS
 CC Mucociliary dysfunction is the inability of ciliated epithelium to clear
 CC mucus and sputum in lung airways. Mucociliary dysfunction is a serious
 CC complication of chronic obstructive lung diseases such as Chronic
 CC Bronchitis (CB), Bronchiectasis (BE), asthma and Cystic Fibrosis (CF).
 CC In addition, patients suffering from mucociliary dysfunction are
 CC susceptible to secondary bacterial infections. A partial coding sequence
 CC for human placental bikunin has been isolated (see AAA70371). Placental
 CC bikunin is a Kunitz-type serine protease inhibitor protein, which can
 CC stimulate the rate of mucociliary clearance of mucus and sputum in lung
 CC airways. Therefore, placental bikunin protein may be used for treating
 CC lung diseases such as CF, CB, BE, and chronic sinusitis and glue ear
 CC which are caused by retention and accumulation of mucus. The present
 CC sequence is an oligonucleotide used to clone the partial human placental
 CC bikunin coding sequence of AAA70371.
 XX
 SQ Sequence 35 BP; 7 A; 9 C; 14 G; 5 T; 0 other;

Query Match 74.0%; Score 14.8; DB 21; Length 35;
 Best Local Similarity 88.9%; Pred. No. 3.9e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 tcctcgtcgtcgtgga 20
 ||||| ||||| |||||
 Db 6 tcctcactcgtcgcgga 23

RESULT 5
 AAT92645/c
 ID AAT92645 standard; DNA; 20 BP.
 XX
 AC AAT92645;
 XX
 DT 22-APR-1998 (first entry)
 XX
 DE B2LF1 gene's specific antisense oligonucleotide 212.

XX Epstein-Barr virus; antisense oligonucleotide; EBV; treatment; tumour;
 KW B2LF1; BRLF1; BMLF1; BLRF1; BYRF1; BHRF1; BSLF2; BSLF2; ss.
 XX
 OS Synthetic.
 OS Epstein-Barr virus.
 PN WO9737669-A1.
 XX
 PD 16-OCT-1997.
 XX
 PF 04-APR-1997; 97WO-US06104.
 XX
 PR 05-APR-1996; 96US-0628422.
 XX
 PA (UYMA-) UNIV MASSACHUSETTS.
 XX
 PI Mulder C;
 XX
 DR WPI: 1997-512403/47.
 XX
 XX Anti-sense oligo:nucleotide(s) that inhibit Epstein-Barr virus
 PT function - used to treat or prevent EB virus infections, including
 PT tumours
 PT
 XX
 PS Claim 5; Page 54; 79pp; English.
 XX
 CC This antisense oligonucleotide is specific to a portion of the B2LF1
 CC gene. Antisense oligonucleotides specific to any of the different
 CC strains of Epstein-Barr virus (EBV) such as the B2LF1, BRLF1, BMLF1,
 CC BRLF1, BMLF1, BYRF1, BHRF1, BSLF2 and terminal proteins 1 and 2
 CC are used to inhibit EBV function. These antisense oligonucleotides are
 CC antisense sequences that inhibit EBV replication or gene expression. The
 CC antisense oligonucleotides or the vectors expressing them, are used to
 CC treat or prevent EBV infection (including tumours such as nasopharyngeal
 CC carcinoma) in mammals. When labelled, they can also be used to detect
 CC cells infected with EBV. The antisense oligonucleotides can be targeted
 CC to either the latent or the lytic phase of the virus cycle. Combinations
 CC of the antisense oligonucleotides directed against different viral genes
 CC may provide a synergistic inhibitory effect. Formulation of these
 CC antisense oligonucleotides with transfection agents can increase the
 CC efficiency and reduce their needed dosage.
 XX
 SQ Sequence 20 BP; 5 A; 7 C; 4 G; 4 T; 0 other;

Query Match 71.0%; Score 14.2; DB 18; Length 20;
 Best Local Similarity 84.2%; Pred. No. 7.1e+02;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 ttctcgtcgtcgtgga 20
 ||||| ||||| |||||
 Db 20 TTGCTCGCAGCTGGAGAA 2

RESULT 6
 AAQ61472/c
 ID AAQ61472 standard; DNA; 18 BP.
 XX
 AC AAQ61472;
 XX
 XX 17-MAY-1994 (first entry)
 DT
 XX
 DE Primer pair #6 Oligo2 to amplify M.tuberculosis katG gene.
 XX
 KW catalase-peroxidase; isonicotinic acid hydrazide; isoniazid; INH;
 KW antibiotic; susceptibility; sensitive; resistant; katG;
 KW polymerase chain reaction; Single strand conformation polymorphism;
 KW PCR-SSCP analysis; ss.
 XX
 OS Synthetic.
 OS
 XX
 XX Key Location/Qualifiers
 FH

```

FT misc_difference 8 /*tag= a
FT FT /note= "letter O printed at this site in the
FT FT specification"
XX
XX WO9322454-A.
XX
XX 11-NOV-1993.
XX
XX 30-APR-1993; 93WO-EP01063.
XX
XX 17-SEP-1992; 92FR-0011098.
XX 30-APR-1992; 92US-0875940.
XX 14-AUG-1992; 92US-0929206.
XX 16-APR-1993; 93FR-0004545.
XX
XX (ASSI-) ASSISTANCE PUBLIQUE.
XX (INSP ) INST PASTEUR.
XX (MEDI-) MEDICAL RES COUNCIL.
XX (UYBE-) UNIV BERNE.
XX (UYPA-) UNIV CURIE PARIS VI P & M.
XX
XX Bodmer T, Cole S, Heym B, Honore N, Telenti A;
XX Young D, Zhang Y;
XX WPI; 1993-368812/46.
XX
XX Rapid detection of antibiotic resistance in Mycobacteria - esp.
XX isoniazid, rifampicin or streptomycin resistance in tuberculosis
XX by detecting mutation in katG, rpoB or rpsL genes
XX
XX Example 2; Page 29; 97pp; English.
XX
XX Eleven pairs of primers were synthesised and used to generate PCR
XX products of around 280bp, that covered the complete katG gene and
XX some of the flanking sequences. With these primers, a panel of
XX INH-resistant strains of M.tuberculosis was examined using PCR-SSCP
XX analysis to localise the katG mutations responsible for isoniazid
XX resistance.
XX
XX Sequence 18 BP; 5 A; 6 C; 5 G; 1 T; 1 other;

Query Match 70.0%; Score 14; DB 14; Length 18;
Best Local Similarity 93.3%; Pred. No. 8.7e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 ctcgctgctgtgga 19
DB 16 CTCGCTGCNGGTGGA 2

RESULT 7
ID AAA58527/c
XX AAA58527 standard; DNA; 18 BP.
XX
XX AAA58527;
XX
XX 20-OCT-2000 (first entry)
XX
XX PCR primer used to amplify bleomycin (BLM) gene cluster ORF34.
XX
XX BLM gene cluster; bleomycin gene cluster; polyketide metabolite;
XX bleomycin; bleomycin analogue; holo-carrier protein; thiazolidine;
XX thiazoline; bithiazoline; microbial metabolite; sugar; PCR primer; ss.
XX
XX Streptomyces verticillus.
XX
XX WO200040704-A1.
XX
XX 13-JUL-2000.
XX
XX 06-JAN-2000; 2000WO-US00445.

XX 06-JAN-1999; 99US-0115435.
XX 05-FEB-1999; 99US-0118848.
XX 05-JAN-2000; 2000US-0477962.
XX
XX (REGC ) UNIV CALIFORNIA.
XX
XX Shen B, Du L, Sanchez C, Chen M, Edwards DJ;
XX
XX WPI; 2000-465974/40.
XX
XX New bleomycin gene cluster components useful for peptide and/or
XX polyketide metabolites, especially bleomycin, production and for
XX chemically modifying biological molecules -
XX
XX Disclosure; Page 22; 162pp; English.
XX
XX PCR primers AAA58474-A58541 were used to amplify open reading frames
XX (ORFs) 8 to 41 of the BLM (Bleomycin) gene cluster. The proteins encoded
XX by the gene cluster are useful for producing peptides and/or polyketide
XX metabolites, especially bleomycin or bleomycin analogues. They are
XX also useful for chemically modifying biological molecules to produce
XX also useful methyl groups, and for coupling amino acids and fatty
XX acids. They may be reacted with an apo-carrier protein and coenzyme A
XX to produce a holo-carrier protein. The BLM gene cluster or catalytic
XX domains can be used individually or collectively to produce
XX thiazolidine, thiazoline, bithiazoline and bithiazoline-containing
XX microbial metabolites. The BLM gene cluster may also be used to produce
XX sugars.
XX
XX Sequence 18 BP; 5 A; 6 C; 5 G; 2 T; 0 other;

Query Match 70.0%; Score 14; DB 21; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ctcgctgctgtggtg 17
DB 17 CCTCGCTGCTGGTG 4

RESULT 8
ID AAAQ88809
XX AAAQ88809 standard; cDNA to mRNA; 32 BP.
XX
XX AAAQ88809;
XX
XX 27-APR-1995 (first entry)
XX
XX BoPCar I, bovine parathyroid calcium receptor PCR primer.
XX
XX BoPCar I; bovine parathyroid calcium receptor; hyperparathyroidism;
XX ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX modified_base 8 /*tag= a
XX modified_base i
XX modified_base 13 /*tag= b
XX modified_base i
XX
XX WO9418959-A.
XX
XX 01-SEP-1994.
XX
XX 23-FEB-1993; 93WO-US01642.
XX
XX 23-FEB-1993; 93AU-0037770.
XX 23-FEB-1993; 93WO-US01642.

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XX (BGHM) BRIGHAM & WOMENS HOSPITAL.
 PA (NPSP-) NPS PHARM INC.
 PI Balandrin MF, Brown EM, Del MAR EG, Fuller FH, Hebert SC;
 PI Nemeth EF, Van WAGENEN BC;
 XX WPI; 1994-293958/36.
 XX Compn. contg. partly new calci-mimetic and calcilytic cpds. -
 PT for treating parathyroidism, Paget's disease etc. and for
 PT diagnosis, also new ion receptors and associated nucleic acid,
 PT antibodies and transgenic animals
 XX Disclosure; Page 100; 283pp; English.
 XX
 XX AAQ88809 was used in combination with AAQ88810 as primers for the
 CC PCR amplification of BopCAR 1, bovine parathyroid
 CC calcium receptor, which was used to test the effectiveness of
 CC new calci-mimetics that mimics the action of extracellular
 CC Ca ions. These calci-mimetics can be used in the treatment
 CC of a variety of diseases associated with abnormal levels of
 CC Ca in cells, blood and plasma, specifically hyperparathyroidism.
 XX Sequence 32 BP; 5 A; 4 C; 8 G; 8 T; 7 other;
 SQ

Query Match 68.0%; Score 13.6; DB 15; Length 32;
 Best Local Similarity 70.0%; Pred. No. 1.4e+03;
 Matches 14; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 attctcgctgctgtgaa 20
 | | | | | | | | | |
 Db 5 actnctgntbctgtggar 24

RESULT 9
 AAX96509/c
 ID AAX96509 standard; DNA; 20 BP.
 XX
 AC AAX96509;
 XX
 XX 13-SEP-1999 (first entry)
 DT
 DE PCR primer used to amplify an ORF of Chlamydia pneumoniae.
 XX
 XX Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
 KW sinusitis; purulent otitis media; erythema nodosum; pharyngitis;
 KW vaccine; neutralising epitope; PCR primer; ss.
 XX
 XX Synthetic.
 OS Chlamydia pneumoniae.
 XX
 XX WO927105-A2.
 PN
 XX 03-JUN-1999.
 PD
 XX 20-NOV-1998; 98WO-IB01890.
 PF
 XX 04-NOV-1998; 98US-0107078.
 PR
 XX 21-NOV-1997; 97FR-0014673.
 XX
 XX (GEST) GENSET.
 PA
 XX Griffais R;
 PI
 XX WPI; 1999-357842/30.
 DR
 XX Genome sequence of Chlamydia pneumoniae
 PT
 XX Page 1831; Disclosure; 1912pp; English.
 PS
 XX AAX91991-X97517 represent PCR primers used to amplify open reading
 CC

CC frames and other nucleic acid sequences from the genome of
 CC Chlamydia pneumoniae (see AAX91990). C. pneumoniae causes respiratory
 CC disease such as pneumonia and bronchitis and is thought to be a
 CC contributing factor in heart disease, sarcoidosis, sinusitis, purulent
 CC otitis media, erythema nodosum or pharyngitis. The polypeptides encoded
 CC by the open reading frames of the C. pneumoniae genome (see AAX34584-
 CC AAY35879) can be used in immunogenic compositions as vaccines. Vectors
 CC containing C. pneumoniae nucleotides sequences can also be used as
 CC immunogenic compositions, especially where the vector directs the
 CC expression of a neutralising epitope of C. pneumoniae.
 XX Sequence 20 BP; 6 A; 4 C; 7 G; 3 T; 0 other;
 SQ

Query Match 67.0%; Score 13.4; DB 20; Length 20;
 Best Local Similarity 93.3%; Pred. No. 1.7e+03;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 attctcgctgctgg 15
 | | | | | | | | | |
 Db 19 ACTCCTCGCTGCTGG 5

RESULT 10
 AAX05609/c
 ID AAX05609 standard; DNA; 26 BP.
 XX
 AC AAX05609;
 XX
 XX 21-APR-1999 (first entry)
 DT
 DE PmerR promoter amplifying reverse primer.
 XX
 XX Erythromycin; oxygen-binding protein; transformation; S. erythraea;
 KW PmerR promoter; Vitreoscilla; haemoglobin; Vhb; PCR primer; ss.
 XX
 XX Synthetic.
 OS Streptomyces sp.
 XX
 XX WO9853084-A1.
 PN
 XX 26-NOV-1998.
 PD
 XX 22-MAY-1998; 98WO-IB00790.
 PF
 XX 22-MAY-1997; 97US-0861450.
 PR
 XX (SOLI-) SOLIDAGO AG.
 PA
 XX Bailey JE, Brunner P, Kallio P, Minas W;
 PI
 XX WPI; 1999-070154/06.
 DR
 XX New organism expressing oxygen-binding protein - useful, e.g. in
 PT methods for highly efficient production of erythromycin
 PT
 XX Example 1; Page 15; 44pp; English.
 PS
 XX The invention provides an erythromycin-producing organism that expresses
 CC a heterologous oxygen-binding protein. The oxygen-binding protein can be
 CC used in a method for increasing erythromycin production that comprises
 CC culture of oxygen-binding protein under erythromycin production
 CC conditions. The method is exemplified by stably transforming
 CC Saccharopolyspora erythraea with an exogenous DNA construct, comprising
 CC directing integration of the construct at the phl C31 attachment site of
 CC the S. erythraea chromosome. The organism and the methods are used to
 CC provide more efficient production of erythromycin. Sequences
 CC AAX05608-609 represent PCR primers used for the amplification of PmerR
 CC promoter. This is used in the construction of expression vectors
 CC containing Vitreoscilla haemoglobin (Vhb) and chromosomal integration of
 CC the Vhb expression cassette in S. erythraea.
 XX
 XX Sequence 26 BP; 6 A; 9 C; 3 G; 8 T; 0 other;
 SQ

Query Match 67.0%; Score 13.4; DB 20; Length 26;
 Best Local Similarity 93.3%; Pred. No. 1.7e+03;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 tcgctgctggtgga 20
 | | | | | | | | | |
 Db 26 TAGCTGCTGGTGGAA 12

RESULT 11
 AAX09838/c
 ID AAX09838 standard; DNA; 20 BP.
 XX AC AAX09838;
 XX DT 24-MAR-1999 (first entry)
 XX DE Human biallelic polymorphic marker downstream primer #144.
 KW Polymorphism: biallelic; human; forensic; paternity testing; disease;
 KW detection; phenotypic typing; characteristic; infection; hereditary;
 KW autoimmune disease; cancer; inflammation; drug; therapy; medicament;
 KW treatment; marker; primer; ss.
 XX OS Synthetic.
 XX OS Homo sapiens.
 XX PN WO9820165-A2.
 XX PD 14-MAY-1998.
 XX PF 05-NOV-1997; 97WO-US20313.
 XX PR 06-NOV-1996; 96US-0030455.
 XX PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
 XX PI Hudson T, Lander ES, Wang D;
 XX WPI: 1998-286974/25.

New isolated nucleic acid segments from the human genome - used for
 determining polymorphic forms for use in e.g. forensics, paternity
 testing or phenotypic typing for disease
 Claim 16; Page 63; 310pp; English.

AAX09121-X10268 are allele-specific oligonucleotide primers used in the
 isolation of various biallelic polymorphic markers found in the human
 genome (represented in AAX10269-X12937). These primers can be used in a
 method for determining polymorphic forms in an individual for use in
 e.g. forensics, paternity testing or for phenotypic typing for diseases
 such as agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome,
 muscular dystrophy, Wiskott-Aldrich syndrome, Fabry's disease, familial
 hypercholesterolemia, polycystic kidney disease, hereditary
 spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary
 haemorrhagic telangiectasia, familial colonic polyposis, Ehlers-Danlos
 syndrome, osteogenesis imperfecta, acute intermittent porphyria,
 autoimmune diseases, inflammation, cancer, diseases of the nervous
 system, infection by pathogenic microorganisms, and characteristics such
 as longevity, appearance (e.g. baldness, obesity), strength, speed,
 endurance, fertility, and susceptibility or receptivity to particular
 drugs or therapeutic treatments. The isolated polymorphic nucleic acid
 segments can also be used to produce medicaments for the treatment or
 prophylaxis of such diseases.

Sequence 20 BP; 8 A; 4 C; 7 G; 1 T; 0 other;

Query Match 66.0%; Score 13.2; DB 19; Length 20;
 Best Local Similarity 83.3%; Pred. No. 2.1e+03;

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 2 ttctcgctgctggtgga 19
 | | | | | | | | | |
 Db 20 TTCCTCTCTTCTCGTGGGA 3

RESULT 12
 AAC87185/c
 ID AAC87185 standard; DNA; 23 BP.
 XX AC AAC87185;
 XX DT 09-MAR-2001 (first entry)
 XX DE Rice mutant EPSPS PCR primer, SEQ ID NO:40.
 KW Rice EPSPS; 5-enolpyruvylshikimate phosphate synthase;
 KW glyphosate resistance; herbicide resistance; transgenic plant;
 KW expression construct; PCR primer; ss.
 XX OS Oryza sativa.
 XX OS Synthetic.
 XX PN WO200066748-A1.
 XX PD 09-NOV-2000.
 XX PF 20-APR-2000; 2000WO-CB01573.
 XX PR 29-APR-1999; 99GB-0009968.
 XX PR 29-APR-1999; 99GB-0017834.
 XX PR 29-APR-1999; 99GB-0030213.
 XX PR 29-JUL-1999; 99GB-0017839.
 XX PR 29-JUL-1999; 99GB-0017840.
 XX PR 29-JUL-1999; 99GB-0017846.
 XX PR 29-JUL-1999; 99GB-0017847.
 XX PR 21-DEC-1999; 99GB-0030200.
 XX PR 21-DEC-1999; 99GB-0030204.
 XX PR 21-DEC-1999; 99GB-0030207.
 XX PR 21-DEC-1999; 99GB-0030209.
 XX PA (ZENE) ZENECA LTD.
 XX PI Hawkes TR, Warner SAJ, Andrews CJ, Bachoo S, Pickerill AP;
 XX WPI: 2000-687544/67.

Novel polynucleotide encoding 5-enolpyruvylshikimate phosphate
 synthase, used to produce transgenic plants e.g. banana, wheat, maize
 or rice, having resistance or tolerance to glyphosate herbicide -
 Example 20; Page 51; 87pp; English.

The invention relates to rice 5-enolpyruvylshikimate phosphate synthase
 (EPSPS) genomic DNA (AAC87188). The invention also relates to an
 expression cassette comprising, in the 5'-3' direction, one or more
 transcriptional enhancer elements selected from AAC87190-C87196), the
 rice EPSPS promoter, genomic DNA encoding a rice EPSPS chloroplast
 transit peptide, genomic DNA encoding a EPSPS protein modified such that
 it is resistant to glyphosate (AAC87189), and a transcriptional
 terminator. The glyphosate resistant EPSPS contains a region (AAB29793)
 containing two amino acid substitutions relative to the corresponding
 wild-type region (AAB29792). The invention also encompasses plant genomic
 EPSPS sequences identified via screening with a rice EPSPS intronic
 sequence; vectors and host plant cells comprising a nucleic acid sequence
 of the invention; transgenic plants (and tissues and seeds thereof)
 comprising a nucleic acid sequence of the invention, optionally further
 transformed with a DNA encoding an insect, fungal, viral, bacterial,
 nematode, stress or herbicide resistance protein; and methods of
 producing the transgenic plants of the invention. The nucleic acids and
 constructs of the invention are used to produce a wide variety of
 morphologically normal, glyphosate resistant plants. The glyphosate

CC resistant plants produced are particularly maize, soybean, cotton,
 CC sugarbeet and canola, but also other field crops, fruits and vegetables,
 CC turf and forage grasses and nut-producing plants. The plants are
 CC optionally resistant to insects, fungi, viruses, bacteria, nematodes,
 CC stress, desiccation and/or other herbicides. They can be used in the
 CC production of a herbicidal target for the high throughput in vitro
 CC screening of potential herbicides. The present sequence represents a PCR
 CC primer used in an exemplification of the invention.

XX Sequence 23 BP; 5 A; 7 C; 5 G; 6 T; 0 other;

Query Match 65.0%; Score 13; DB 21; Length 23;
 Best Local Similarity 100.0%; Pred. No. 2.6e+03;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 gctgctggtgga 20
 |||||

Db 20 GCTGCTGGTGGA 8

RESULT 13

AAC88395/c
 ID AAC88395 standard; DNA; 23 BP.

XX AAC88395;

DT 02-MAR-2001 (first entry)

DE Primer Universal reverse.

XX Glyphosate; 5-enolpyruvylshikimate phosphate synthase; EPSPS;
 KW herbicide resistance; ss.

XX Synthetic.

XX WO200066746-A1.

XX 09-NOV-2000.

XX 20-APR-2000; 2000WO-GB01559.

XX 29-APR-1999; 99GB-0009971.

XX 29-APR-1999; 99GB-0009972.

XX 29-JUL-1999; 99GB-0017837.

XX 29-JUL-1999; 99GB-0017842.

XX 21-DEC-1999; 99GB-0030190.

XX 21-DEC-1999; 99GB-0030206.

XX 21-DEC-1999; 99GB-0030214.

XX 21-DEC-1999; 99GB-0030216.

XX (ZENE) ZENECA LTD.

XX Hawkes TR, Warner SAJ, Andrews CJ, Bachoo S, Pickerill AP;

XX WPI; 2000-679763/66.

XX Novel polynucleotide encoding the rice 5-enolpyruvylshikimate phosphate
 CC synthase, used to produce glyphosate tolerant or resistant plants -
 CC Example 20; Page 50; 85pp; English.

XX The present invention relates to a glyphosate resistant rice
 CC 5-enolpyruvylshikimate phosphate synthase (EPSPS) gene. This gene can
 CC be used to produce plant tissue and/or morphologically normal fertile
 CC whole plants which are tolerant or resistant to glyphosate herbicide,
 CC and in the production of a herbicidal target for the high throughput
 CC in vitro screening of potential herbicides.

XX Sequence 23 BP; 5 A; 7 C; 5 G; 6 T; 0 other;

Query Match

65.0%; Score 13; DB 21; Length 23;

Best Local Similarity 100.0%; Pred. No. 2.6e+03;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 gctgctggtgga 20
 |||||

Db 20 GCTGCTGGTGGA 8

RESULT 14

AAC89319/c
 ID AAC89319 standard; DNA; 23 BP.

XX AAC89319;

DT 07-MAR-2001 (first entry)

DE Primer universal reverse.

XX 5-enolpyruvylshikimate phosphate synthase; EPSPS;
 KW herbicide resistance; glyphosate; ss.

XX Synthetic.

XX WO200066747-A1.

XX 09-NOV-2000.

XX 20-APR-2000; 2000WO-GB01572.

XX 29-APR-1999; 99GB-0009967.

XX 29-APR-1999; 99GB-0009969.

XX 29-APR-1999; 99GB-0009972.

XX 29-APR-1999; 99GB-0009981.

XX 29-APR-1999; 99GB-0017835.

XX 29-JUL-1999; 99GB-0017836.

XX 29-JUL-1999; 99GB-0017843.

XX 21-DEC-1999; 99GB-0030202.

XX 21-DEC-1999; 99GB-0030210.

XX 21-DEC-1999; 99GB-0030212.

XX (ZENE) ZENECA LTD.

XX Hawkes TR, Warner SAJ, Andrews CJ, Bachoo S, Pickerill AP;

XX WPI; 2000-679764/66.

XX Isolated polynucleotide encoding a 5-enolpyruvylshikimate phosphate
 CC synthase from rice is used for producing transgenic plants with
 CC enhanced resistance to glyphosate herbicide -
 CC Example 20; Page 49; 98pp; English.

XX The present invention relates to an Oryza sp. 5-enolpyruvylshikimate
 CC phosphate synthase (EPSPS) gene. Vectors containing the gene may be
 CC used to produce plant tissues and fertile whole plants which are
 CC substantially tolerant or substantially resistant to glyphosate
 CC herbicide and to produce a herbicidal target which is used for high
 CC throughput in vitro screening of potential herbicides.

XX Sequence 23 BP; 5 A; 7 C; 5 G; 6 T; 0 other;

Query Match

65.0%; Score 13; DB 21; Length 23;
 Best Local Similarity 100.0%; Pred. No. 2.6e+03;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 gctgctggtgga 20
 |||||

Db 20 GCTGCTGGTGGA 8

RESULT 15

AAA82953/c

ID AAA82953 standard; DNA; 19 BP.
XX
AC AAA82953;
XX
DT 04-DEC-2000 (first entry)
XX
DE cdk6 ribozyme binding site #13.
XX
KW Ribozyme; hairpin; hammerhead; gene therapy; vasotropic;
KW restenosis; ss.
XX
OS Mammalia.
XX
PN WO200032765-A2.
XX
PD 08-JUN-2000.
XX
PF 06-DEC-1999; 99WO-US28772.
XX
PR 04-DEC-1998; 98US-0110954.
XX
PA (IMMU-) IMMUSOL INC.
XX
PI Tritz R, Welch PJ, Barber JR, Robbins JM;
XX
DR WPI; 2000-412314/35.
XX
PT New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves
PT RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,
PT PCNA and Cyclin B1
XX
PS Disclosure; Page 54; 109pp; English.
XX
CC The present invention relates to a hairpin or hammerhead ribozyme,
CC designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase
CC other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.
CC Representative examples of ribozyme recognition sites are given in
CC AAA82415 to AAA86787. The ribozyme of the invention is useful for
CC inhibiting restenosis by introduction of the ribozyme into cells.
CC The ribozyme is resistant to endonuclease activity and hence is
CC efficient in restenosis treatment.
XX
SQ Sequence 19 BP; 3 A; 8 C; 5 G; 3 T; 0 other;

Query Match 64.0%; Score 12.8; DB 21; Length 19;
Best Local Similarity 87.5%; Pred. No. 3.2e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 cctcgtcgtgtgga 19
| | | | | | | | | |
Db 17 CCTCGGGGATGGGA 2

Search completed: October 2, 2001, 16:18:45
Job time: 15489 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 2, 2001, 16:03:51 ; Search time 417.38 Seconds
(without alignments)
9.071 Million cell updates/sec

Title: US-09-757-100B-16

Perfect score: 20

Sequence: 1 ctaggaggagctcagtggtgg 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 324599 seqs, 9465562 residues

Total number of hits satisfying chosen parameters: 460742

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_NA.*

1: /cgn2_6/ptodata/1/ina/5A_COMB.seq.*

2: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*

3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*

4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*

5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq.*

6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	3	US-09-377-310-16
2	15	75.0	15	3	US-09-377-310-36
c 3	13.2	66.0	18	2	US-08-585-684B-2592
c 4	13.2	66.0	18	4	US-09-038-073-2592
5	13.2	66.0	20	3	US-09-166-186-87
6	13.2	66.0	20	4	US-09-313-932-87
c 7	13.2	66.0	47	1	US-08-171-389-275
c 8	13.2	66.0	47	1	US-08-123-936-275
c 9	13.2	66.0	47	2	US-08-475-228A-275
c 10	13.2	66.0	47	3	US-08-482-080A-275
c 11	13.2	66.0	47	5	PCT-US93-12388-275
c 12	12.8	64.0	30	1	US-08-049-283A-21
c 13	12.8	64.0	47	1	US-08-171-389-285
14	12.8	64.0	47	1	US-08-123-936-285
15	12.8	64.0	47	1	US-08-475-228A-285
16	12.8	64.0	47	3	US-08-482-080A-285
17	12.8	64.0	47	5	PCT-US93-12388-285
c 18	12.6	63.0	28	2	US-08-477-890-2
c 19	12.6	63.0	28	2	US-08-467-034A-2
c 20	12.6	63.0	28	4	US-08-468-646A-2
21	12.6	63.0	29	3	US-08-792-108A-3
c 22	12.6	63.0	31	3	US-08-929-140-14
c 23	12.6	63.0	32	1	US-08-246-123C-2
c 24	12.6	63.0	32	2	US-08-751-233A-2
c 25	12.6	63.0	33	1	US-07-834-539A-76
c 26	12.6	63.0	33	2	US-08-800-353-76
27	12.6	63.0	49	1	US-07-960-982-23

c 28	12.4	62.0	30	1	US-08-049-283A-22	Sequence 22, Appl
29	12.4	62.0	30	3	US-08-881-037-81	Sequence 81, Appl
c 30	12.2	61.0	26	1	US-07-796-106-16	Sequence 16, Appl
31	12	60.0	29	1	US-08-418-859-31	Sequence 31, Appl
32	12	60.0	29	1	US-08-418-859-32	Sequence 32, Appl
33	12	60.0	29	2	US-08-643-181-31	Sequence 31, Appl
34	12	60.0	29	2	US-08-643-181-32	Sequence 32, Appl
c 35	12	60.0	33	4	US-08-943-529-1	Sequence 1, Appl
36	12	60.0	38	2	US-08-839-581A-23	Sequence 23, Appl
37	12	60.0	38	4	US-08-023-591A-23	Sequence 23, Appl
38	12	60.0	40	1	US-08-050-132A-11	Sequence 11, Appl
39	12	60.0	40	3	US-08-815-652B-11	Sequence 11, Appl
c 40	11.8	59.0	19	1	US-08-602-036A-17	Sequence 17, Appl
c 41	11.8	59.0	19	2	US-08-502-374A-17	Sequence 17, Appl
c 42	11.8	59.0	19	2	US-08-642-407A-17	Sequence 17, Appl
c 43	11.8	59.0	22	3	US-08-928-881-12	Sequence 12, Appl
c 44	11.8	59.0	23	1	US-08-189-237-5	Sequence 5, Appl
45	11.8	59.0	26	1	US-07-834-539A-77	Sequence 77, Appl

ALIGNMENTS

RESULT 1

US-09-377-310-16

; Sequence 16, Application US/09377310B

; Patent No. 6133031

; GENERAL INFORMATION:

; APPLICANT: Monia, Brett P.

; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase

; FILE REFERENCE: ISPH-0389

; CURRENT APPLICATION NUMBER: US/09/377,310B

; CURRENT FILING DATE: 1999-08-19

; NUMBER OF SEQ ID NOS: 43

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 16

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: antisense sequence

US-09-377-310-16

Query Match 100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ctaggaggagctcagtggtgg 20

|||||

Db 1 ctaggaggagctcagtggtgg 20

RESULT 2

US-09-377-310-36

; Sequence 36, Application US/09377310B

; Patent No. 6133031

; GENERAL INFORMATION:

; APPLICANT: Monia, Brett P.

; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase

; FILE REFERENCE: ISPH-0389

; CURRENT APPLICATION NUMBER: US/09/377,310B

; CURRENT FILING DATE: 1999-08-19

; NUMBER OF SEQ ID NOS: 43

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 36

; TYPE: DNA

; ORGANISM: Artificial Sequence

```

; FEATURE:
; OTHER INFORMATION: antisense sequence
US-09-377-310-36

```

Query Match 75.0%; Score 15; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 15; Conservative 0; Mismatches 0; Indels

Qy 3 aggggaggtcagtq 17
| | | | | | | | | |
Db 1 aggggaggtcagtq 15

```

RESULT      3
US-08-585-684B-2592/c
; Sequence 2592, Application US/08585684B
; Patent No. 5877021
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Daniel T.
; APPLICANT: Jarvis, Thale
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE
; TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES
; NUMBER OF SEQUENCES: 2751
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.

```

Query Match 66.0%; Score 13.2; DB 2; Length 18;
Best Local Similarity 83.3%; Pred. No. 3.4e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ctaggggaggctcagtg 18
||| ||||| ||| |||
Db 18 CTGGGGGAGGCTGAGGGT 1

RESULT 4

```

US-09-038-073-2592/c
: Sequence 2592, Application US/09038073
: Patent No. 6194150
: GENERAL INFORMATION:
: APPLICANT: Stinchcomb, Daniel T.
: APPLICANT: Jarvis, Thale
: APPLICANT: McSwiggan, James
: TITLE OF INVENTION: METHOD AND REAGENT FOR THE
: TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE
: TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES
: NUMBER OF SEQUENCES: 2751
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Lyon & Lyon
: STREET: 633 West Fifth Street
: STREET: Suite 4700
: CITY: Los Angeles
: STATE: California
: COUNTRY: U.S.A.
: ZIP: 90071
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
: MEDIUM TYPE: storage
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: IBM P.C. DOS 5.0
: SOFTWARE: FastSeq Version 1.5
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/038,073
: FILING DATE:
: PRIORITY APPLICATION DATA:
: APPLICATION NUMBER: 08/585,684
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Warburg, Richard
: REGISTRATION NUMBER: 32,327
: REFERENCE/DOCKET NUMBER: 218/078
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (213) 489-1600
: TELEFAX: (213) 955-0440
: TELEX: 67-3510
: INFORMATION FOR SEQ ID NO: 2592:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 18 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
US-09-038-073-2592

```

Query Match 66.0%; Score 13.2; DB 4; Length 18;
Best Local Similarity 83.3%; Pred. No. 3.4e+02;
Matches 15; Conservative 0; Mismatches 3; Indels

Qy 1 ctaggggaggctcagtg 18
|||
Db 18 CTGGGGGAGGCTGAGGGT 1

```

RESULT 5
US-09-166-87-186
; Sequence 87: Application US/09166186A
; Patent No. 6080580
; GENERAL INFORMATION:
; APPLICANT: Baker, Brenda
; APPLICANT: Bennett, C. Frank
; APPLICANT: Butler, Madeline M.
; APPLICANT: Shanahan, William R.
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES
; FILE REFERENCE: ISPH-0322
; CURRENT APPLICATION NUMBER: US/09/166-87-186
; CURRENT FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 250
; SEQ ID NO 87
; LENGTH: 20

```

RESULT 4

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/996,783
FILING DATE: 23-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/723,618
FILING DATE: 27-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 4600-0075.32/G19P2
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 275:
SEQUENCE CHARACTERISTICS:
LENGTH: 47 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Human estrogen-responsive gene ps2
US-08-123-936-275

Query Match 66.0%; Score 13.2; DB 1; Length 47;
Best Local Similarity 83.3%; Pred. No. 3.6e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 tagggaggctcagtgtg 19
||||| ||||| |||||

Db 22 TAGGCAGGCTCTGTTG 5

RESULT 9
US-08-475-228A-275/c
Sequence 275, Application US/08475228A
Patent No. 5869241
GENERAL INFORMATION:
APPLICANT: Edwards, Cynthia A.
APPLICANT: Cantor, Charles R.
APPLICANT: Andrews, Beth M.
APPLICANT: Turin, Lisa M.
APPLICANT: Fry, Kirk E.
TITLE OF INVENTION: Sequence-Directed DNA Binding
NUMBER OF SEQUENCES: 664
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genelabs Technologies, Inc.
STREET: 505 Penobscot Drive
CITY: Redwood City
STATE: CA
COUNTRY: USA
ZIP: 94063
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,228A
FILING DATE: 06-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/123,936
FILING DATE: 17-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/996,783
FILING DATE: 23-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/723,618
FILING DATE: 27-JUN-1991

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/081,070
FILING DATE: 22-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 4600-0175.21/G19P3D2
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 275:
SEQUENCE CHARACTERISTICS:
LENGTH: 47 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Human estrogen-responsive gene ps2
US-08-475-228A-275

Query Match 66.0%; Score 13.2; DB 2; Length 47;
Best Local Similarity 83.3%; Pred. No. 3.6e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 tagggaggctcagtgtg 19
||||| ||||| |||||

Db 22 TAGGCAGGCTCTGTTG 5

RESULT 10
US-08-482-080A-275/c
Sequence 275, Application US/08482080A
Patent No. 6010849
GENERAL INFORMATION:
APPLICANT: Edwards, Cynthia A.
APPLICANT: Cantor, Charles R.
APPLICANT: Andrews, Beth M.
APPLICANT: Turin, Lisa M.
APPLICANT: Fry, Kirk E.
TITLE OF INVENTION: Sequence-Directed DNA Binding
NUMBER OF SEQUENCES: 664
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genelabs Technologies, Inc.
STREET: 505 Penobscot Drive
CITY: Redwood City
STATE: CA
COUNTRY: USA
ZIP: 94063
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,080A
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/171,389
FILING DATE: 20-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/123,936
FILING DATE: 17-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/996,783
FILING DATE: 23-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/723,618
FILING DATE: 27-JUN-1991

```
; APPLICATION NUMBER: US 08/081,070
; FILING DATE: 22-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Brady, John F.
; REGISTRATION NUMBER: 39,118
; REFERENCE/DOCKET NUMBER: 4600-0175.20/G19P3D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 324-0880
; TELEFAX: (650) 324-0960
; INFORMATION FOR SEQ ID NO: 275:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 47 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: Human estrogen-responsive gene p52
; US-08-482-080A-275

Query Match 66.0%; Score 13.2; DB 3; Length 47;
Best Local Similarity 83.3%; Pred. No. 3.6e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 tagggaggctcagtgtg 19
||||| ||||| |||
Db 22 TAGGGCAGGCTCTGTTG 5

RESULT 11
PCT-US93-12388-275/c
; Sequence 275, Application PC/TUS9312388
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Sequence-Directed DNA Binding
; TITLE OF INVENTION: Molecules, Compositions and Methods
; NUMBER OF SEQUENCES: 641
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genelabs Technologies, Inc.
; STREET: 505 Penobscot Drive
; CITY: Redwood City
; STATE: CA
; COUNTRY: USA
; ZIP: 94063
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/12388
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/123,936
; FILING DATE: 17-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/996,783
; FILING DATE: 23-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Fabian, Gary R.
; REGISTRATION NUMBER: 33,875
; REFERENCE/DOCKET NUMBER: 4600-0175.41/G19PCT2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 275:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 47 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
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; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: Human estrogen-responsive gene p52
; PCT-US93-12388-275

Query Match 66.0%; Score 13.2; DB 5; Length 47;
Best Local Similarity 83.3%; Pred. No. 3.6e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 tagggaggctcagtgtg 19
||||| ||||| |||
Db 22 TAGGGCAGGCTCTGTTG 5

RESULT 12
US-08-049-283A-21/c
; Sequence 21, Application US/08049283A
; Patent No. 5502176
; GENERAL INFORMATION:
; APPLICANT: Tenen, Daniel G.
; APPLICANT: Pahl, Heike L.
; APPLICANT: Burn, Timothy C.
; TITLE OF INVENTION: Cell Specific Promoter and Uses Thereof
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/049,283A
; FILING DATE: 14-APR-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/020,465
; FILING DATE: 19-FEB-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/837,776
; FILING DATE: 13-FEB-1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: BIH91-03/A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-049-283A-21

Query Match 64.0%; Score 12.8; DB 1; Length 30;
Best Local Similarity 87.5%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 ggggaggctcagtgtg 19
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Query Match	64.08;	Score 12.8;	DB 1;	Length 47;
Best Local Similarity	87.5%;	Pred. No. 5.7e+02;		
Matches 14;	Conservative	0;	Mismatches 2;	Indels 0; Gaps 0;
Qy	3	aggggaggctcagtgt	18	
Db	8	AGGGAAGGCTCAGTAT	23	

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Query Match      64.0%; Score 12.8; DB 1; Length 47;
Best Local Similarity 87.5%;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      3 aggggagggctcagtgt 18
          |||| ||||| |||
Db       8 AGGGAAGGCTCAGTAT 23

```

RESULT 15
US-08-475-228A-285
; Sequence 285, Application US/08475228A
; Patent No. 5869241
; GENERAL INFORMATION:
; APPLICANT: Edwards, Cynthia A.
; APPLICANT: Cantor, Charles R.
; APPLICANT: Andrews, Beth M.
; APPLICANT: Turin, Lisa M.

APPLICANT: Fry, Kirk E.
TITLE OF INVENTION: Sequence-Directed DNA Binding
TITLE OF INVENTION: Molecules, Compositions and Methods
NUMBER OF SEQUENCES: 664
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genelabs Technologies, Inc.
STREET: 505 Penobscot Drive
CITY: Redwood City
STATE: CA
COUNTRY: USA
ZIP: 94063
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,228A
FILING DATE: 06-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/123,936
FILING DATE: 17-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/996,783
FILING DATE: 23-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/723,618
FILING DATE: 27-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/081,070
FILING DATE: 22-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 4600-0175.21/G19P3D2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 285:
SEQUENCE CHARACTERISTICS:
LENGTH: 47 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Human SAAL beta gene
US-08-475-228A-285

Query Match 64.08; Score 12.8; DB 2; Length 47;
Best Local Similarity 87.5%; Pred. No. 5.7e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 agggaggagctcagtg 18
|||||
Db 8 AGGGAAGGCTCAGTAT 23

Search completed: October 2, 2001, 16:03:51
Job time: 14595 sec

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: October 2, 2001, 16:18:43 ; Search time 876.95 Seconds

(without alignments)

14.320 Million cell updates/sec

Title: US-09-757-100B-16

Perfect score: 20

Sequence: 1 ctaggaggagctcagtgtgg 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 730101 seqs, 313950809 residues

Total number of hits satisfying chosen parameters: 854978

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- N_Geneseq_0601:*
- 1: /SIDS8/gcgdata/geneseq/geneseq/NA1980.DAT:*
 - 2: /SIDS8/gcgdata/geneseq/geneseq/NA1981.DAT:*
 - 3: /SIDS8/gcgdata/geneseq/geneseq/NA1982.DAT:*
 - 4: /SIDS8/gcgdata/geneseq/geneseq/NA1983.DAT:*
 - 5: /SIDS8/gcgdata/geneseq/geneseq/NA1984.DAT:*
 - 6: /SIDS8/gcgdata/geneseq/geneseq/NA1985.DAT:*
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 - 9: /SIDS8/gcgdata/geneseq/geneseq/NA1988.DAT:*
 - 10: /SIDS8/gcgdata/geneseq/geneseq/NA1989.DAT:*
 - 11: /SIDS8/gcgdata/geneseq/geneseq/NA1990.DAT:*
 - 12: /SIDS8/gcgdata/geneseq/geneseq/NA1991.DAT:*
 - 13: /SIDS8/gcgdata/geneseq/geneseq/NA1992.DAT:*
 - 14: /SIDS8/gcgdata/geneseq/geneseq/NA1993.DAT:*
 - 15: /SIDS8/gcgdata/geneseq/geneseq/NA1994.DAT:*
 - 16: /SIDS8/gcgdata/geneseq/geneseq/NA1995.DAT:*
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 - 18: /SIDS8/gcgdata/geneseq/geneseq/NA1997.DAT:*
 - 19: /SIDS8/gcgdata/geneseq/geneseq/NA1998.DAT:*
 - 20: /SIDS8/gcgdata/geneseq/geneseq/NA1999.DAT:*
 - 21: /SIDS8/gcgdata/geneseq/geneseq/NA2000.DAT:*
 - 22: /SIDS8/gcgdata/geneseq/geneseq/NA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	22	AAC65548 Human focal adhesi
2	15	75.0	15	22	AAC65568 Human focal adhesi
3	13.4	67.0	34	17	AAT18223 HBEGF DNA antisens
4	13.4	67.0	35	17	AAT18225 HBEGF DNA antisens
5	13.2	66.0	18	17	Human B7-2 hairpin
6	13.2	66.0	20	21	AAA40846 Human TNFalpha ant
7	13.2	66.0	21	22	AAC90428 Human clone p12616
8	13.2	66.0	33	18	AAT91995 Primer for human c
9	13.2	66.0	47	15	AA069525 Human estrogen-res
10	13.2	66.0	47	18	AAT63987 Human oestrogen-re
11	13.2	66.0	47	20	AA17275 Test sequence from

12	12.8	64.0	21	22	AAF96616 Human gene single
13	12.8	64.0	25	21	AAC66790 Human hyperpolaris
14	12.8	64.0	30	17	AAT14576 CD11b gene promote
15	12.8	64.0	43	16	AA104232 pNIV3606 amplifica
16	12.8	64.0	47	15	AA069535 Human SAA1 beta ge
17	12.8	64.0	47	18	AAT63997 Human SAA1 beta ge
18	12.8	64.0	47	20	AAX17285 Test sequence from
19	12.6	63.0	27	17	AAX35053 HSV thymidine kina
20	12.6	63.0	28	19	AAV19540 Recombinant retrov
21	12.6	63.0	29	21	AA10258 Fibrinogen B-beta
22	12.6	63.0	31	20	AA103879 PCR primer for bet
23	12.6	63.0	32	18	AAT58070 Potyvirus p1 prote
24	12.6	63.0	32	20	AAZ23620 Reporter gene cons
25	12.6	63.0	32	21	AAC66808 Oligo "g" used in
26	12.6	63.0	33	20	AA106060 Hygromycin phospho
27	12.6	63.0	35	18	AA159277 Hygromycin phospho
28	12.6	63.0	35	20	AA158529 Hygromycin phospho
29	12.4	62.0	25	19	AAV39103 Primer CYP2DEIR us
30	12.4	62.0	30	13	AAQ25680 Sequence of 5' LH p
31	12.4	62.0	30	17	AAT14577 CD11b gene promote
32	12.4	62.0	42	21	AA158778 PCR primer for Fv
33	12.4	62.0	42	21	AA158779 PCR primer for Fv
34	12.2	61.0	20	22	AAC60289 Primer R2 used to
35	12.2	61.0	25	21	AAC66789 Human hyperpolaris
36	12.2	61.0	26	14	AAQ34833 PCR primer #1 to a
37	12.2	61.0	30	19	AAV11129 SH2 binding protei
38	12.2	61.0	34	20	AA17216 Constitutatory pro
39	12.2	61.0	34	21	AA250600 3' B7-2 primer to
40	12	60.0	16	22	AA172764 Human HIV-1 monocl
41	12	60.0	21	20	AA129888 Primer OS295 for m
42	12	60.0	25	21	AA151454 Human NK2R promote
43	12	60.0	29	14	AAQ37256 Minisatellite MS32
44	12	60.0	29	14	AAQ37257 Minisatellite MS32
45	12	60.0	29	17	AAT40160 MS32 minisatellite

ALIGNMENTS

RESULT 1

AAC65548

ID AAC65548 standard; DNA; 20 BP.

XX AC

XX AAC65548;

DT 12-FEB-2001 (first entry)

XX XX

DE Human focal adhesion kinase antisense sequence #14.

XX XX

KW Human; focal adhesion kinase; FAK; signal transduction; cancer;

KW embryonic development disorder; angiogenic disorder; wound healing;

KW antisense; phosphorothioate; ss.

XX OS Homo sapiens.

XX XX

PN US6133031-A.

XX PD 17-OCT-2000.

XX PF 19-AUG-1999; 99US-0377310.

XX PR 19-AUG-1999; 99US-0377310.

XX (ISIS-) ISIS PHARM INC.

PA Monia BP, Gaarde WA;

PI WPI; 2001-006141/01.

DR New antisense compounds for inhibiting focal adhesion kinase

XX PT expression, especially useful for inhibiting retinal

XX PT neovascularization, or for diagnosing and treating e.g. colon cancer -

XX XX

PS Claim 3; Column 23; 30pp; English.

XX The present invention describes a number of phosphorothioate antisense
CC sequences to the human focal adhesion kinase (FAK) protein. This protein
CC is involved in integrin-mediated signal transduction, and is implicated
CC in cancer, particularly colon, breast and oral tumours, embryonic
CC development disorders, angiogenic disorders and wound healing. The
CC antisense sequences, including the one shown here, can be used in the
CC treatment of all of these.

XX Sequence 20 BP; 3 A; 3 C; 10 G; 4 T; 0 other;

Query Match 100.0%; Score 20; DB 22; Length 20;

Best Local Similarity 100.0%; Pred. No. 0.53; Mismatches 0; Gaps 0;

Matches 20; Conservative 0; Indels 0; Indels 0; Gaps 0;

Qy 1 ctaggggaggctcagtggtg 20

Db 1 ctaggggaggctcagtggtg 20

RESULT 2

AAC65568 AAC65568 standard; DNA; 15 BP.

XX AAC65568;

DT 12-FEB-2001 (first entry)

XX Human focal adhesion kinase antisense sequence #34.

XX Human; focal adhesion kinase; FAK; signal transduction; cancer;
KW embryonic development disorder; angiogenic disorder; wound healing;
KW antisense; phosphorothioate; ss.

XX Homo sapiens.

XX US6133031-A.

PD 17-OCT-2000.

PF 19-AUG-1999; 990S-0377310.

PR 19-AUG-1999; 990S-0377310.

XX (ISIS-) ISIS PHARM INC.

XX Monia BP, Gaarde WA;

XX WPI; 2001-006141/01.

XX New antisense compounds for inhibiting focal adhesion kinase
PT expression, especially useful for inhibiting retinal
PT neovascularization, or for diagnosing and treating e.g. colon cancer -

PS Example 2; Column 25; 30pp; English.

XX The present invention describes a number of phosphorothioate antisense
CC sequences to the human focal adhesion kinase (FAK) protein. This protein
CC is involved in integrin-mediated signal transduction, and is implicated
CC in cancer, particularly colon, breast and oral tumours, embryonic
CC development disorders, angiogenic disorders and wound healing. The
CC antisense sequences, including the one shown here, can be used in the
CC treatment of all of these.

XX Sequence 15 BP; 3 A; 2 C; 8 G; 2 T; 0 other;

Query Match

Best Local Similarity 75.0%; Score 15; DB 22; Length 15;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 aggggaggctcagtg 17

Db 1 aggggaggctcagtg 15

RESULT 3

AAT18223 AAT18223 standard; DNA; 34 BP.

XX AAT18223;

DT 24-JUN-1996 (first entry)

XX HBEGF DNA antisense primer.

XX HBEGF; heparin-binding epidermal-like growth factor; saporin;
KW cytotoxic; ribosome-inactivating protein; targeted delivery; tumour;
KW breast cancer; bladder cancer; restenosis; therapy; primer; PCR;
KW polymerase chain reaction; ss.

XX Synthetic.

XX WO9608274-A2.

XX 21-MAR-1996.

XX 13-SEP-1995; 95WO-US12205.

PR 16-MAY-1995; 95US-0441979.

PR 13-SEP-1994; 94US-0305771.

XX (PRIZ-) PRIZM PHARM INC.

XX Chandler LA, Houston LL, McDonald JR, Nova MP, Sosnowski BA;

XX WPI; 1996-179728/18.

XX Conjugate comprising HBEGF polypeptide and targeted agent - used to
PT treat HBEGF-mediated patho:physiological conditions, e.g. solid
PT tumour and skin disorders

XX Example 6; Page 94; 163pp; English.

XX Sense and antisense PCR primers (AAT18222-23) were used to amplify
CC DNA (see AAT17958) coding for human heparin-binding epidermal-like
CC growth factor (HBEGF) (AAR92897) using p232B1 as template. The
CC PCR product has a 5' NcoI site and a 3' stop codon followed by
CC an SalI site. It was ligated into PETSAP-MCS (see AAT18220-21).
CC The resulting plasmid (p236B1) (see AAT18232) codes for a fusion
CC (AAR92921) of HBEGF and saporin linked by an Ala-Met-Ala linker.
CC This was expressed in Escherichia coli and is useful for targeting
CC cytotoxic saporin e.g. to solid tumour cells bearing the HBEGF
CC receptor.

XX Sequence 34 BP; 9 A; 8 C; 9 G; 8 T; 0 other;

Query Match 67.0%; Score 13.4; DB 17; Length 34;

Best Local Similarity 93.3%; Pred. No. 9e+02;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ctaggggaggctcag 15

Db 11 ctatgggaggctcag 25

RESULT 4

AAT18225 AAT18225 standard; DNA; 35 BP.

XX AAT18225;

DT 24-JUN-1996 (first entry)

```

XX DE HBEGF DNA antisense primer.
XX PF
XX PR
KW HBEGF: heparin-binding epidermal-like growth factor; saporin;
KW cytotoxic; ribosome-inactivating protein; targeted delivery; tumour;
KW breast cancer; bladder cancer; restenosis; therapy; primer; PCR;
XX polymerase chain reaction; baculovirus; ss.
XX OS
XX PN Synthetic.
XX PD WO9608274-A2.
XX PR 21-MAR-1996.
XX PF 13-SEP-1995; 95WO-US12205.
XX PR 16-MAY-1995; 95US-0441979.
XX PR 13-SEP-1994; 94US-0305771.
XX PA (PRIZ-) PRIZM PHARM INC.
XX PI Chandler LA, Houston LL, McDonald JR, Nova MP, Sosnowski BA;
XX WPI; 1996-179728/18.
XX DR
XX PR Conjugate comprising HBEGF polypeptide and targeted agent - used to
XX treat HBEGF-mediated patho:physiological conditions, e.g. solid
XX tumour and skin disorders
XX PS
XX Example 8; Page 96; 163pp; English.
XX CC
XX CC An antisense PCR primer (AAT18225) was used with sense primers
XX (AAT18224 or AAT18227) to amplify DNA (see AAT17958) coding for
XX human heparin-binding epidermal-like growth factor (HBEGF)
XX (AAR92897) using p3281 as template. The PCR products were
XX ligated into pBlueac111 (Invitrogen) (see AAT18226 and AAT18228)
XX and used for baculovirus expression of HBEGF. Conjugates of
XX HBEGF with saporin are useful for targeted treatment of e.g.
XX solid tumours.
XX CC
XX Sequence 35 BP; 10 A; 8 C; 8 G; 9 T; 0 other;
XX SQ

Query Match 67.0%; Score 13.4; DB 17; Length 35;
Best Local Similarity 93.3%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ctatggggaggctcag 15
   ||| |||||
Db 12 ctatggggaggctcag 26

RESULT 5
AAX67092/c
ID AAX67092 standard; RNA; 18 BP.
XX AC
XX AAX67092;
XX DT 20-JUL-1999 (first entry)
XX DE
XX Human B7-2 hairpin ribozyme target SEQ ID NO:3724.
XX KW
XX Arthritic condition; graft tolerance; immune response; target; cleavage;
XX hammerhead ribozyme; hairpin ribozyme; human; rabbit; mouse; collagenase;
XX stromelysin; synovial membrane; joint; arthritis; osteoarthritis;
XX rheumatoid arthritis; autoimmune disease; allergy; inflammation;
XX diagnosis; ss.
XX OS
XX Homo sapiens.
XX PN WO9618736-A2.
XX PD 20-JUN-1996.

XX XX 22-NOV-1995; 95WO-US15516.
XX PF
XX PR 05-OCT-1995; 95US-0541365.
XX PR 13-DEC-1994; 94US-0354920.
XX PR 23-DEC-1994; 94US-0363253.
XX PR 23-DEC-1994; 94US-0363254.
XX PR 17-FEB-1995; 95US-0390850.
XX PR 20-APR-1995; 95US-0426124.
XX PR 02-MAY-1995; 95US-0432874.
XX PR 04-MAY-1995; 95US-0434509.
XX PR 07-JUL-1995; 95US-0000951.
XX PR 07-JUL-1995; 95US-0000974.
XX PR 07-AUG-1995; 95US-0512861.
XX PA (RIBO-) RIBOZYME PHARM INC.
XX PI Draper K, Gustofson J, McSwiggen J, Pavco P, Stinchcomb DT;
XX PI Beigelman L, Karpeisky A, Modak A, Usman N, Burgin A;
XX PI Matulic-Adamic J, Jarvis T, Thompson JD, Wincott F;
XX DR
XX WPI; 1996-300653/30.
XX CC
XX Enzymatic nucleic acid molecules having a hammer-head motif - used
XX for the treatment of arthritis, induction of graft tolerance or
XX treatment of auto-immune diseases
XX Claim 10; Page 216; 307pp; English.
XX CC
XX The present invention describes a novel enzymatic nucleic acid (ENA)
XX having a hammerhead motif (HM) comprising: (i) at least 5 ribose
XX residues; (ii) a 2'-C-allyl modification at position 4 of the ENA; (iii)
XX at least ten 2'-O-methyl modifications; and (iv) a 3'-end modification.
XX The ENA's can inhibit collagenase and stromelysin production in the
XX synovial membrane of joints for the treatment or prevention of arthritis,
XX particularly osteoarthritis or rheumatoid arthritis. The ENA's can also
XX be used to treat antigen presenting cells of a donor to induce tolerance
XX in a recipient to an alloantigen of a donor. They can also be used for
XX enhancing graft tolerance or for treating autoimmune disease, and for
XX treating allergies and other inflammatory conditions. The ENA's can also
XX be used in diagnosis. Ribozyme therapy impacts on the expression of
XX stromelysin without introducing the non-specific effects upon gene
XX expression which accompany treatment with retinoids and dexamethasone.
XX The concentration of ribozyme required to affect a therapeutic treatment
XX is lower than that required of antisense molecules, and is highly
XX specific. The present sequence is used in the exemplification of the
XX present invention.
XX SQ
Sequence 18 BP; 3 A; 11 C; 2 G; 2 U; 0 other;

Query Match 66.0%; Score 13.2; DB 17; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ctatggggaggctcagtg 18
   || ||||| |||
Db 18 CTGGGGGAGGCTGAGGT 1

RESULT 6
AAX40846
ID AAX40846 standard; DNA; 20 BP.
XX AC
XX AAX40846;
XX DT 16-AUG-2000 (first entry)
XX DE
XX Human TNFalpha antisense oligonucleotide ISIS# 21706.
XX KW
XX Antisense oligonucleotide; phosphorothioate; TNFalpha; cytokine; inhibit;
XX tumour necrosis factor alpha; inflammatory bowel disease; diabetes;
XX rheumatoid arthritis; infectious disease; multiple sclerosis; hepatitis;

```

KW pancreatitis; atopic dermatitis; allograft rejection;
 KW autoimmune disease; inflammatory disease; ss.
 XX
 OS Synthetic.

XX
 PN WO200020645-A1.
 XX
 XX 13-APR-2000.

XX
 PD 05-OCT-1999; 99WO-US23205.
 XX
 PF 05-OCT-1998; 98US-0166186.
 XX
 PR 18-MAY-1999; 99US-0313932.
 XX
 XX (ISIS-) ISIS PHARM INC.

XX
 PA Baker BF, Bennett CF, Butler MM, Shanahan WJ;
 XX
 PI WPI; 2000-303808/26.
 XX
 DR Oligonucleotide for treating diseases associated with human tumour
 XX necrosis factor-alpha (TNFalpha) such as, diabetes and rheumatoid
 XX arthritis, comprises nucleotide sequence complementary to intron of
 XX nucleic acid encoding TNFalpha -

XX
 PS Example 6; Page 58; 283pp; English.

XX This sequence represents an antisense oligonucleotide sequence which
 CC targets a region of the human tumour necrosis factor alpha (TNFalpha)
 CC nucleotide sequence. TNFalpha is an important cytokine that plays a role
 CC in host defence. It is produced mainly in macrophages and monocytes in
 CC response to infection, invasion, injury or inflammation. Overexpression
 CC of TNFalpha can result in disease states, particularly in infectious,
 CC inflammatory and autoimmune diseases. The invention relates to antisense
 CC oligonucleotides, such as that represented by the present sequence which
 CC are capable of modulating the TNFalpha gene expression. The
 CC oligonucleotides optionally have a phosphorothioate backbone, and may
 CC also optionally contain at least one 2'-O-methoxyethyl modification. The
 CC oligonucleotides are useful for modulating the expression of human
 CC TNFalpha in cells and tissues, reducing a human cell inflammatory
 CC response, reducing the blood glucose level in a human and treating a
 CC human having a disease or condition associated with TNFalpha. Examples of
 CC diseases associated with TNFalpha include diabetes, inflammatory bowel
 CC disease, multiple sclerosis, pancreatitis, rheumatoid arthritis,
 CC infectious disease, hepatitis, atopic dermatitis or allograft rejection.
 CC The antisense oligonucleotides are also useful for modulating the
 CC function of a selected nucleic acid sequence in adipose tissue.

XX
 XX Sequence 20 BP; 5 A; 3 C; 9 G; 3 T; 0 other;

Query Match 66.0%; Score 13.2; DB 21; Length 20;
 Best Local Similarity 83.3%; Pred. No. 1.1e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 agggggaggtcagtggtg 20
 || |||| |||||
 Db 1 agaggagagtcagtggtg 18

RESULT 7

AAC90428/c

ID AAC90428 standard; DNA; 21 BP.

XX
 AC AAC90428;

XX
 XX 19-MAR-2001 (first entry)

XX
 DT Human clone p12616HY PCR primer #1.

XX
 DE Human; clone p12616HY; immune response modulation; autoimmune disorder;
 KW inflammatory response; hematopoiesis; gene therapy; allergy; PCR primer;
 KW autoimmune disorder; tissue repair; wound healing; chemokine;

KW chromosome 2q11; ss.

XX
 OS Homo sapiens.

XX
 PN WO200073320-A1.

XX
 XX 07-DEC-2000.

XX
 XX 25-MAY-2000; 2000WO-US14572.

XX
 PR 27-MAY-1999; 99US-0322134.

XX
 PA (HYSE-) HYSEQ INC.

XX
 PI Ford J, Yeung G;

XX
 XX WPI; 2001-041140/05.

XX New chemokine polypeptide from fetal liver-spleen, useful in gene
 XX therapy, especially for modulating hematopoiesis, or immune or
 XX inflammatory responses, e.g. for repairing tissues or treating
 XX autoimmune disorders -

XX
 PS Example 3; Page 78; 92pp; English.

XX The present sequence is a PCR primer for human clone AAP12616HY coding
 CC sequence (see AAC90427). The AAP12616HY coding sequence is useful for
 CC modulating the immune and inflammatory responses, and hematopoiesis; and
 CC in gene therapy for treating allergies (e.g. asthma), autoimmune
 CC disorders (e.g. arthritis or transplantation rejection), in tissue
 CC repair and replacement, or wound healing (e.g. treatment of burns,
 CC treatment of surgical incisions and ulcers, such as stomach or diabetic
 CC ulcers). The AAP12616HY coding sequence is thought to encode a chemokine
 CC and is located on chromosome 2q11.

XX
 XX Sequence 21 BP; 7 A; 7 C; 4 G; 3 T; 0 other;

Query Match 66.0%; Score 13.2; DB 22; Length 21;
 Best Local Similarity 83.3%; Pred. No. 1.1e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 agggggaggtcagtggtg 20
 || |||| |||||
 Db 19 AGTGCAGTCTCAGTGTGG 2

RESULT 8

AAT91995/c

ID AAT91995 standard; DNA; 33 BP.

XX
 AC AAT91995;

XX
 DT 08-APR-1998 (first entry)

XX
 XX Primer for human chemokine alpha-3 cDNA.

XX Human; chemokine alpha-3; CK alpha-3; treatment; tumour;
 KW chronic infection; leukaemia; T-cell mediated autoimmune disease;
 KW parasitic infection; psoriasis; asthma; allergy; hematopoiesis;
 KW growth factor; angiogenesis; wound healing; PCR primer; ss.

XX
 OS Synthetic.

XX
 OS Homo sapiens.

XX
 PN WO9735027-A1.

XX
 XX 25-SEP-1997.

XX
 PF 18-MAR-1996; 96WO-US03686.

XX
 PR 18-MAR-1996; 96WO-US03686.

PA (HUMA-) HUMAN GENOME SCI INC.
 XX Li H, Ni J, Su JY;
 XX WPI; 1997-480232/44.
 XX Polynucleotide(s) encoding human chemokine alpha-3 - used to treat
 PT tumours, chronic infections, autoimmune diseases, parasitic
 PT infections, psoriasis, asthma etc.
 XX Example 3; Page 54; 69pp; English.
 XX The present sequence is a primer for the cDNA encoding human
 CC chemokine alpha-3 (CK alpha-3). CK alpha-3 can be used to treat
 CC tumours, chronic infections, leukaemia, T-cell mediated autoimmune
 CC diseases, parasitic infections, psoriasis, asthma and allergy. It
 CC can also be used to regulate haematopoiesis, stimulate growth
 CC factor activity, inhibit angiogenesis and promote wound healing.
 XX Sequence 33 BP; 8 A; 14 C; 7 G; 4 T; 0 other;
 SQ

Query Match 66.08; Score 13.2; DB 18; Length 33;
 Best Local Similarity 83.3%; Pred. No. 1.1e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 agggaggctcagtggtg 20
 | | | | | | | | | |
 Db 28 ACGGAGGCTCATGTGG 11

RESULT 9
 AAQ69525/C
 ID AAQ69525 standard; DNA; 47 BP.
 XX
 AC AAQ69525;
 XX
 XX
 DT 01-MAR-1995 (first entry)
 XX
 DE Human estrogen-responsive gene pS2 target region.
 XX
 KW DNA protein-binding assay; test sequence; screening sequence;
 KW promoter; target; TATA box; Herpes Simplex Virus; HSV;
 KW origin of replication; UL9; transcription factor; TFIID: ds.
 XX
 OS Synthetic.
 XX
 PN W09414980-A.
 XX
 XX
 PD 07-JUL-1994.
 XX
 XX
 PF 20-DEC-1993; 93WO-US12388.
 XX
 XX
 PR 23-DEC-1992; 92US-0996783.
 XX
 PR 17-SEP-1993; 93US-0123936.
 XX
 XX
 PA (GENE-) GENELABS TECHNOLOGIES INC.
 XX
 PI Andrews BM, Cantor CR, Edwards CA, Fry KE, Turin LM;
 XX
 XX WPI; 1994-234711/28.
 XX
 XX Sequence-directed DNA-binding molecules - useful in
 PT pharmaceuticals and as molecular reagents
 XX
 XX Claim 28; Page 349; 587pp; English.
 XX
 XX A DNA protein-binding assay is provided, useful for screening
 CC libraries of synthetic or biological cnds. for their ability
 CC to bind DNA test sequences. The assay is versatile in that any
 CC number of test sequences can be tested by placing the test sequence
 CC adjacent to a defined protein-binding screening sequence. Binding
 CC of mols. to these test sequences changes the binding characteristics

of the protein mol. to its cognate binding sequence. When such a mol.
 binds the test sequence, the equilibrium of the DNA:protein complexes
 is disturbed, generating changes in the concentration of free DNA probe.
 One application of this method is to eucaryotic general transcription
 factors (e.g. TFIID), where the target region is typically selected
 from DNA sequences adjacent to the binding site for the eucaryotic
 CC transcription factor. Numerous exemplary test sequences are given:
 CC the sequences in AAQ69251-731 and AAQ69850 correspond to promoter
 CC targets (typically, TATA box-contg. sites) for human genes and the
 CC sequences in AAQ69732-849 correspond to promoter targets for viral genes.
 CC The test sequences may also be randomly generated. DNA:protein
 CC interaction may be used for screening purposes, e.g. the Herpes Simplex
 CC virus (HSV) origin of replication and UL9 (see AAQ69851-52, AAQ69865 and
 CC AAQ69891).
 XX
 SQ Sequence 47 BP; 12 A; 15 C; 13 G; 7 T; 0 other;
 Query Match 66.08; Score 13.2; DB 15; Length 47;
 Best Local Similarity 83.3%; Pred. No. 1.2e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 tagggaggctcagtggtg 19
 | | | | | | | | | |
 Db 22 TAGGCGAGGCTCTGTGG 5

RESULT 10
 AAT63987/C
 ID AAT63987 standard; DNA; 47 BP.
 XX
 AC AAT63987;
 XX
 XX
 DT 17-MAR-1997 (first entry)
 XX
 DE Human oestrogen-responsive gene, pS2, TFIID binding site.
 XX
 KW Duplex DNA; target region; binding characteristic; DNA binding protein;
 KW TFIID; transcription factor; binding site; inhibition; enhance;
 KW inherited genetic disorder; cancer; ds.
 XX
 OS Homo sapiens.
 XX
 XX
 PN US5578444-A.
 XX
 XX 26-NOV-1996.
 PD
 XX
 XX 27-JUN-1991; 91US-0723618.
 XX
 XX 20-DEC-1993; 93US-0171389.
 PR
 XX 27-JUN-1991; 91US-0723618.
 PR
 XX 23-DEC-1992; 92US-0996783.
 PR
 XX 17-SEP-1993; 93US-0123936.
 XX
 XX
 PA (GENE-) GENELABS TECHNOLOGIES INC.
 XX
 XX Andrews BM, Cantor CR, Edwards CA, Fry KE, Turin LM;
 XX
 XX WPI; 1997-020402/02.
 XX
 XX Altering binding characteristics of DNA binding proteins to duplex
 PT DNA - by attaching specific small cpd. to target region close to the
 PT protein's binding site, useful in treatment of viral disease, cancer
 PT etc
 XX
 XX Claim 6; Column 239-240; 264pp; English.
 XX
 XX The sequences given in AAT63713-4312 represent duplex DNA's which act
 CC as target regions in the method of the invention. The method for
 CC altering the binding characteristics of a DNA-binding protein to duplex
 CC DNA comprises contacting the duplex DNA with a small molecule which
 CC binds sequence-specifically to a target region, where, when the small
 CC molecule is bound to the target region, it is adjacent to, but not

CC overlapping by more than 4 bp, a binding site for a DNA-binding protein.
 CC The small molecule is added at a concentration effective to alter the
 CC binding of the DNA binding protein, pref. TFIID, to its binding site on
 CC the duplex DNA. The binding of the small molecule may inhibit or
 CC enhance the binding of the DNA-binding protein to its binding site. The
 CC compounds isolated using this method are potentially useful as
 CC therapeutic agents for treatment of any disease which involves a
 CC specific DNA sequence, e.g. cancer, or inherited genetic disorders etc.
 CC The method is suitable for screening large biological or chemical
 CC libraries and allows determination of sequence-specific and relative
 CC affinities of known DNA-binding agents for different DNA sequences.
 CC The design of these duplex DNA's allows a single DNA:protein interaction
 CC to be used for screening sequence-specific, or preferential, DNA binding
 CC proteins that recognise almost any possible sequence (see also AAT49539-
 CC 74).

XX
 SQ Sequence 47 BP; 12 A; 15 C; 13 G; 7 T; 0 other;

Query Match 66.0%; Score 13.2; DB 18; Length 47;
 Best Local Similarity 83.3%; Pred. No. 1.2e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 taggggaggtcagtg 19
 ||||| ||||| || ||
 Db 22 TAGGGCAGGCTCTGTTG 5

RESULT 11
 AAX17275/C
 ID AAX17275 standard; DNA; 47 BP.
 XX
 AC AAX17275;
 XX
 DT 06-MAY-1999 (first entry)
 XX
 DE Test sequence from human estrogenresponsive gene pS2.

XX Test sequence; DNA-binding molecule; screening sequence; human;
 KW nucleic acid amplification; target; viral; ds.
 XX
 OS Homo sapiens.

XX US5869241-A.
 PN
 XX 09-FEB-1999.
 PD
 XX 07-JUN-1995; 95US-0475228.
 PF

XX 20-DEC-1993; 93US-0171389.
 PR 27-JUN-1991; 91US-0723618.
 PR 23-DEC-1992; 92US-0996783.
 PR 17-SEP-1993; 93US-0123936.
 PR 07-JUN-1995; 95US-0475228.

XX (GENE-) GENELABS TECHNOLOGIES INC.
 PA

XX Andrews BM, Cantor CR, Edwards CA, Fry KE, Turin LM;
 PI WPI; 1999-152755/13.

XX Determination of DNA sequence preference of a DNA-binding molecule -
 PT based on inhibition of binding of protein to oligonucleotide
 PT sequence attached to test sequence

XX Claim 3; Columns 241-242; 270pp; English.

XX Sequences AAX17001 to AAX17600 represent specifically claimed target
 CC test sequences that are used in the method of the invention of
 CC determining the DNA sequence preference of a DNA-binding molecule. The
 CC method comprises: (i) adding a test molecule and a DNA-binding protein to
 CC a mixture of duplex DNA test oligonucleotides, each of the test
 CC oligonucleotides having a test sequence adjacent to a screening sequence,

CC where the screening sequence binds to the DNA-binding protein with a
 CC binding affinity that is independent of the DNA sequence of the test
 CC sequence, and where the mixture of duplex DNA test oligonucleotides
 CC includes several test sequences; (ii) incubating the test molecule, the
 CC mixture of duplex DNA test oligonucleotides and the DNA-binding protein
 CC for a time sufficient to permit binding of the test molecule to test
 CC sequences in the duplex DNA; (iii) separating unbound test
 CC oligonucleotides from test oligonucleotides bound to binding protein;
 CC (iv) amplifying the unbound test oligonucleotides; (v) repeating steps
 CC (ii) to (iv); (vi) isolating the amplified test oligonucleotides; and
 CC (vii) sequencing the isolated test oligonucleotides. Test sequences
 CC AAX17001-X17481 and AAX17600 correspond to promoter targets for human
 CC genes and test sequences AAX17482-X17599 correspond to promoter targets
 CC for viral genes.

XX
 SQ Sequence 47 BP; 12 A; 15 C; 13 G; 7 T; 0 other;

Query Match 66.0%; Score 13.2; DB 20; Length 47;
 Best Local Similarity 83.3%; Pred. No. 1.2e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 taggggaggtcagtg 19
 ||||| ||||| || ||
 Db 22 TAGGGCAGGCTCTGTTG 5

RESULT 12

AAF96616
 ID AAF96616 standard; DNA; 21 BP.

XX
 AC AAF96616;
 XX

XX 06-JUN-2001 (first entry)
 DT
 XX

XX Human gene single nucleotide polymorphism #1377.
 DE

XX Human; variant thrombospondin 1; variant thrombospondin 4; SNP;
 KW polymorphism; vascular disease; coronary artery disease; forensics;
 KW myocardial infarction; atherosclerosis; stroke; venous thromboembolism;

XX pulmonary embolism; paternity test; ds.
 XX
 OS Homo sapiens.

XX
 FH Key Location/Qualifiers
 FT Variation replace(11,C)
 FT /*tag=
 FT /standard_name= "single nucleotide polymorphism"

XX WO200118250-A2.
 PN

XX 15-MAR-2001.
 PD

XX 07-SEP-2000; 2000WO-US24503.
 PF

XX 10-SEP-1999; 99US-0153357.
 PR 26-JUL-2000; 2000US-0220947.

PR 16-AUG-2000; 2000US-0225724.
 PR

XX (WHED) WHITEHEAD INST BIOMEDICAL RES.
 PA (MILL-) MILLENNIUM PHARM INC.

XX Lander ES, Gargill M, Ireland JS, Bolk S, Daley GO, McCarthy JJ;
 PI WPI; 2001-226749/23.

XX Nucleic acids comprising single nucleotide polymorphisms, useful in
 PT applications such as forensics, paternity testing, medicine, genetic
 PT analysis and phenotype correlations to diseases such as diabetes and
 PT atherosclerosis -

XX Examples; Page 142; 242pp; English.
 PS
 XX

CC The present invention provides a method of diagnosing a vascular disease
 CC in an individual, involving determining the sequence at various
 CC polymorphic sites within the human thrombospondin 1 and thrombospondin 4
 CC genes. The sequences at a number of polymorphic sites are also provided
 CC in the specification. In particular, the method can be used in the
 CC diagnosis of atherosclerosis, myocardial infarction, coronary heart
 CC disease, stroke, peripheral vascular diseases, venous thromboembolism
 CC and pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also
 CC useful in forensics, paternity testing, genetic analysis and phenotype
 CC correlations to diseases. The present sequence is an example of one of
 CC the human gene SNPs shown in the specification.

XX Sequence 21 BP; 5 A; 2 C; 12 G; 2 T; 0 other;

Query Match 64.0%; Score 12.8; DB 22; Length 21;
 Best Local Similarity 87.5%; Pred. No. 1.7e+03;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 gggaggtcagtggtg 20
 ||||| |||||
 Db 6 gggaggtcagtggtg 21

RESULT 13
 AAC66790/c
 ID AAC66790 standard; cDNA; 25 BP.

XX AAC66790;

DT 16-FEB-2001 (first entry)

DE Human hyperpolarisation-activated channel HAC3 PCR primer #11.

KW Human; hyperpolarisation-activated channel; HAC3; neuroleptic; nootropic;
 KW cerebrotective; antimigraine; antiarrhythmic; gene therapy;
 KW pacemaker dysfunction; familial sinus rhythm disease;
 KW sick sinus syndrome associated with atrial fibrillation;
 KW sinus tachycardia; bradycardia; ventricular arrhythmia; bipolar disease;
 KW schizophrenia; central nervous system disorder; migraine; seizure;
 KW stroke; PCR primer; ss.

XX Homo sapiens.

XX WO200063349-A1.

PD 26-OCT-2000.

PF 13-APR-2000; 2000WO-US09865.

PR 15-APR-1999; 99US-0129456.

XX (ICAG-) ICAGEN INC.

PI Jegla TJ;

DR WPI; 2000-679592/66.

XX Novel human hyperpolarization activated channel 3 polypeptide useful to
 PT identify hyperpolarization-activated cation channels modulators for
 PT treating familial sinus rhythm diseases, and ventricular arrhythmias -
 XX Example; Page 63; 81pp; English.

XX The present invention relates to the coding sequence and polypeptide
 CC sequence for human hyperpolarisation activated channel 3 (HAC3) (see
 CC AAC66779 and AAB28375). HAC3 comprises an alpha-subunit of a cation
 CC channel, which forms upon hyperpolarisation, a cation channel with an
 CC additional HAC. Modulators of HAC activity are useful for treating
 CC various pacemaker dysfunctions such as familial sinus rhythm diseases,
 CC sick sinus syndrome associated with atrial fibrillation, sinus
 CC tachycardias and bradycardias as well as ventricular arrhythmias. The
 CC modulators are also useful for treating other disorders involving

CC abnormal ion flux, e.g., memory and learning disorders, sleeping
 CC disorders, bipolar disease, schizophrenia, central nervous system (CNS)
 CC disorders such as migraines, hearing and vision problems, seizures, and
 CC as neuroprotective agents (e.g. to prevent stroke). The Human HAC3 coding
 CC sequence is useful for treating the disorders by gene therapy. The
 CC present sequence is a PCR primer which can be used to isolate the human
 CC HAC3 coding sequence.

XX Sequence 25 BP; 4 A; 15 C; 2 G; 4 T; 0 other;

Query Match 64.0%; Score 12.8; DB 21; Length 25;
 Best Local Similarity 87.5%; Pred. No. 1.7e+03;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 gggaggtcagtggtg 20
 ||||| |||||
 Db 18 GGGAGGCTGAGAGTGG 3

RESULT 14
 AAT14576/c
 ID AAT14576 standard; DNA; 30 BP.

XX AAT14576;

AC 24-SEP-1996 (first entry)

XX CD11b gene promoter nucleotides -78 to -49 (wt-78).

XX promoter; myeloid-specific; CD11b; Spl; PU.1; transcription factor;
 KW binding; transcription start site; ss.

XX Homo sapiens.

XX US5502176-A.

PD 26-MAR-1996.

XX 13-FEB-1992; 92US-0837776.

PR 14-APR-1993; 93US-0049283.

PR 13-FEB-1992; 92US-0837776.

PR 19-FEB-1993; 93US-0020465.

XX (BETH-) BETH ISRAEL HOSPITAL BOSTON ASSOC.

XX Burn TC, Pahl HL, Tenen DG;

DR WPI; 1996-179337/18.

XX CD11b gene promoter directing gene expression pref. in myeloid cells
 PT - directs expression in transient transfection assays in transgenic
 PT animals, used to identify factors regulating myeloid cell-specific
 PT transcription

XX Example 10; Column 25-26; 70pp; English.

XX An electrophoretic mobility shift assay (EMSA) was used to investigate
 CC DNA/protein interactions in the CD11b promoter. Nuclear extracts from
 CC U937 (myeloid) or HeLa (non-myeloid) cells were incubated with a 130 bp
 CC probe which extends from bp -90 to +40 of the CD11b promoter. In
 CC addition to the 130 bp probe, 30 bp double stranded oligonucleotides
 CC were used as probes (AAT14576-79). The sequence between bp -64 and -59
 CC constitutes a consensus binding site for the transcription factor Spl,
 CC so to investigate whether complexes formed in the EMSA represent Spl
 CC binding, a 97 bp DNA fragment of the tissue plasminogen promoter contg.
 CC 2 characterised Spl binding sites was used as a competitor. The
 CC complexes, but not the PU.1 complex, were competed by the addition
 CC of DNA contg. Spl binding sites, indicating that they represent Spl
 CC binding the CD11b promoter.

XX Sequence 30 BP; 2 A; 13 C; 5 G; 10 T; 0 other;

Query Match 64.0%; Score 12.8; DB 17; Length 30;
Best Local Similarity 87.5%; Pred. No. 1.8e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 gggggagctcagtg 19
| | | | | | | | | |
DB 18 GCGGAGGCTCAGTGAG 3

RESULT 15

AAT04232/C
ID AAT04232 standard; DNA: 43 BP.

XX
AC AAT04232;

DT 10-JAN-1996 (first entry)

DE PNIV3606 amplification primer #1.

XX Polymerase chain reaction; PCR; primer: amplify; histamine H1 receptor;
KW human; bovine; transformation; drug screening; PNIV3604B;
KW calcium ion mobilisation; inositol 1,4,5-triphosphate; CHO cell;
KW guanine nucleotide regulatory protein; G protein; hybridisation; ss.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT misc_feature 14..43

FT /*tag= a

FT /note= "corresponds to bases 1 to 48 of human histamine
H1 DNA"

XX GB283239-A.

XX PD 03-MAY-1995.

XX PF 29-OCT-1993; 93GB-0022353.

XX PR 29-OCT-1993; 93GB-0022353.

XX PA (UNIO) UCB SA.

XX PI Bollen A, Gillard M, Moguilevsky N, Noyer M, Varsalona F;

XX WPI; 1995-157301/21.

XX PT New nucleic acid encoding human histamine H1 receptor - useful
XX diagnostically and for screening receptor binding drugs

XX PS Example 3; Page 39; 49pp; English.

XX CC This sequence, and the sequence represented by AAT04233 are
XX amplification primers for PNIV3606 (which contains human histamine H1
XX receptor cDNA up to the fourth transmembrane region). The sequences shown
XX in AAT04227, and AAT79965 represent human histamine H1 receptor cDNA and
XX encoded receptor protein, and were constructed using AAT04234-6.
XX Histamine H1 receptor is part of a family of histamine receptor proteins.
XX Of these sequences the greatest homology was found with bovine histamine
XX H1 receptor (overall identity of 82%, with the transmembrane regions
XX alone having an identity of 96%). These receptors are coupled to
XX different second messenger pathways via guanine nucleotide regulatory
XX proteins (G proteins). This receptor transduces the signal through
XX calcium ion mobilisation via an increase in intracellular inositol
XX 1,4,5-triphosphate levels. Plasmids containing human histamine H1
XX receptor cDNA (pref. PNIV3604B) are used to transform mammalian cells
XX (pref. CHO cells). These transformed cells express the receptor on the
XX cell surface. The transformed cells can then be used to identify ligands
XX that bind to the encoded protein, esp. for drug screening. This sequence
XX is also used to detect complementary mRNA in the cell by hybridisation.

XX SQ Sequence 43 BP; 10 A; 17 C; 4 G; 12 T; 0 other;

Query Match 64.0%; Score 12.8; DB 16; Length 43;
Best Local Similarity 87.5%; Pred. No. 1.8e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 taggggaggtcagtg 17
| | | | | | | | | |
DB 27 TTGGGGAGGCTCATTG 12

1

Search completed: October 2, 2001, 16:18:44
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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run On: October 2, 2001, 16:03:50 ; Search time 417.38 Seconds
(without alignments)
9.071 Million cell updates/sec

Title: US-09-757-100B-15

Perfect score: 20

Sequence: 1 tgttggtttccaatcgacc 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 324599 seqs, 9465562 residues

Total number of hits satisfying chosen parameters: 460742

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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- 1: /cgn2_6/ptodata/1/ina/5A_COMB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	3	US-09-377-310-15
2	15	75.0	15	3	US-09-377-310-35
3	13.4	67.0	30	3	US-08-513-974B-129
C 4	12	60.0	30	1	US-08-295-676A-8
C 5	12	60.0	30	2	US-08-948-591-8
6	11.8	59.0	24	2	US-08-612-857-9
7	11.8	59.0	35	1	US-08-612-895A-29
8	11.8	59.0	35	3	US-09-093-293-29
9	11.8	59.0	35	5	PCT-US94-10562A-29
C 10	11.8	59.0	39	4	US-09-163-444-8
C 11	11.6	58.0	34	2	US-08-765-783A-42
C 12	11.6	58.0	34	3	US-08-921-100-42
C 13	11.6	58.0	34	3	US-08-880-142-42
C 14	11.6	58.0	34	3	US-08-902-201-42
C 15	11.6	58.0	34	4	US-09-416-557-42
C 16	11.6	58.0	41	3	US-08-813-507-97
17	11.4	57.0	28	2	US-08-859-998-979
18	11.2	56.0	24	4	US-08-855-146-12
C 19	11.2	56.0	25	3	US-09-083-603B-12
C 20	11.2	56.0	26	1	US-08-752-238-12
C 21	11.2	56.0	34	1	US-08-428-733A-47
C 22	11.2	56.0	37	2	US-08-873-479-54
C 23	11	55.0	18	3	US-09-163-162-19
C 24	11	55.0	18	4	US-09-286-407-19
C 25	11	55.0	21	1	US-08-266-080B-7
26	11	55.0	21	3	US-08-513-974B-262
27	11	55.0	21	3	US-08-513-974B-266

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28      11 55.0      21 3 US-08-513-974B-271
c 29      11 55.0      21 5 PCT-US95-05423-7
30      11 55.0      23 4 US-09-268-140-29
31      11 55.0      30 4 US-09-550-338-10
c 32      11 55.0      31 1 US-08-656-984A-36
c 33      11 55.0      33 3 US-08-468-846-7
34      11 55.0      33 3 US-08-840-062-10
35      11 55.0      36 1 US-07-937-609-12
36      11 55.0      36 3 US-08-936-632B-38
37      11 55.0      36 4 US-08-029-170-12
c 38      11 55.0      36 4 US-08-582-333A-90
c 39      11 55.0      40 1 US-08-443-957-7
c 40      11 55.0      40 2 US-08-581-543-30
c 41      11 55.0      45 1 US-08-171-382-10
c 42      11 55.0      47 2 US-08-031-538-6
43      10.8      30 3 US-08-513-974B-150
44      10.8      31 1 US-08-450-384-8
45      10.8      31 1 US-08-450-384-9

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ALIGNMENTS

RESULT 1

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US-09-377-310-15
; Sequence 15, Application US/09377310B
; Patent No. 6133031
; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P.
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
; FILE REFERENCE: ISPH-0389
; CURRENT APPLICATION NUMBER: US/09/377,310B
; CURRENT FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
US-09-377-310-15

```

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Query Match      100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.035;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 tgttggtttccaatcgacc 20
| | | | | | | | | | | | | | | | | |

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Db 1 tgttggtttccaatcgacc 20
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RESULT 2

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US-09-377-310-35
; Sequence 35, Application US/09377310B
; Patent No. 6133031
; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P.
; APPLICANT: Gaarde, William A.
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
; FILE REFERENCE: ISPH-0389
; CURRENT APPLICATION NUMBER: US/09/377,310B
; CURRENT FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 35
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence

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; FEATURE:
; OTHER INFORMATION: antisense sequence
US-09-377-310-35

Query Match 75.0%; Score 15; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 ttggtttccaatcg 17
|||||
Db 1 ttggtttccaatcg 15

RESULT 3

US-08-513-974B-129
; Sequence 129, Application US/08513974B
; Patent No. 6114139

; GENERAL INFORMATION:

; APPLICANT: Hinuma, Shuji
; APPLICANT: Hosoya, Masaki
; APPLICANT: Fujii, Ryo
; APPLICANT: Ohtaki, Tetsuya
; APPLICANT: Fukusumi, Shoji
; APPLICANT: Ohgi, Kazuhiro

; TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
; NUMBER OF SEQUENCES: 380
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
; STREET: 130 Water Street
; CITY: Boston

; STATE: MA

; COUNTRY: USA

; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/513,974B

; FILING DATE: 14-SEP-1995

; CLASSIFICATION: 536

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/JP95/01599

; FILING DATE: 10-AUG-1995

; APPLICATION NUMBER: JP 7-093989

; FILING DATE: 19-AUG-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: JP 7-057186

; FILING DATE: 16-MAR-1995

; APPLICATION NUMBER: JP 7-007177

; FILING DATE: 20-JAN-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: JP 6-326611

; FILING DATE: 28-DEC-1994

; APPLICATION NUMBER: JP 6-270017

; FILING DATE: 02-NOV-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: JP 6-236357

; FILING DATE: 30-SEP-1994

; APPLICATION NUMBER: JP 6-236356

; FILING DATE: 30-SEP-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: JP 6-189274

; FILING DATE: 11-AUG-1994

; APPLICATION NUMBER: JP 6-189273

; FILING DATE: 11-AUG-1945
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-189272
; FILING DATE: 11-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Resnick, David S.
; REGISTRATION NUMBER: 34,235
; REFERENCE/DOCKET NUMBER: 45753

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617-523-3400

; TELEFAX: 617-523-6440

; INFORMATION FOR SEQ ID NO: 129:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 30 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; MOLECULE TYPE: cdna

US-08-513-974B-129

Query Match 67.0%; Score 13.4; DB 3; Length 30;

Best Local Similarity 93.3%; Pred. No. 1.2e+02;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ttgttggtttccaatc 15

|||||

Db 10 TGTGTTTCCAAC 24

RESULT 4

US-08-295-676A-8/c

; Sequence 8, Application US/08295676A

; Patent No. 5677172

; GENERAL INFORMATION:

; APPLICANT:

; TITLE OF INVENTION: A method for production of proteins in

; NUMBER OF SEQUENCES: 21

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Birch, Stewart, Kolasch and Birch

; STREET: P.O. Box 747

; CITY: Falls Church

; STATE: VA

; COUNTRY: USA

; ZIP: 22040-0747

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/295,676A

; FILING DATE: 09-SEPT-1994

; INFORMATION FOR SEQ ID NO: 8:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 30 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: 5..10

; OTHER INFORMATION: /function= "KpnI restriction site"

; NAME/KEY:

; LOCATION: 1..30

; OTHER INFORMATION: /label= oligonucleotide

; OTHER INFORMATION: /note= "synthetic 5' primer used to create

; OTHER INFORMATION: recognition sites"

US-08-295-676A-8

Query Match 60.0%; Score 12; DB 1; Length 30;
Best Local Similarity 75.0%; Pred. No. 6.6e+02;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 tgggtgttccaatcgacc 20
||||| ||| |||
DB 24 TGTGTTCACAAAGGTACC 5

RESULT 5

US-08-948-591-8/c
Sequence 8, Application US/08948591
Patent No. 5939287

GENERAL INFORMATION:

APPLICANT: A method for production of proteins in yeast
TITLE OF INVENTION: Yeast
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch and Birch
STREET: P.O. Box 747
CITY: Falls Church
STATE: VA
COUNTRY: USA
ZIP: 22040-0747

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/948,591

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/295,676

FILING DATE: 09-SEPT-1994

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 30 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

FEATURE:

NAME/KEY: misc.feature

LOCATION: 5..10

OTHER INFORMATION: /function= "kpnI restriction site"

FEATURE:

NAME/KEY: -

LOCATION: 1..30

OTHER INFORMATION: /label= oligonucleotide

OTHER INFORMATION: /note= "synthetic 5' primer used to create

OTHER INFORMATION: recognition sites"

US-08-948-591-8

Query Match 60.0%; Score 12; DB 2; Length 30;
Best Local Similarity 75.0%; Pred. No. 6.6e+02;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 tgggtgttccaatcgacc 20
||||| ||| |||
DB 24 TGTGTTCACAAAGGTACC 5

RESULT 6

US-08-612-857-9

Sequence 9, Application US/08612857

Patent No. 5831048

GENERAL INFORMATION:

APPLICANT: SCHWEIGHOFFER, Fabien

APPLICANT: TOCQUE, Bruno
TITLE OF INVENTION: GRB3-3 GENE, VARIANTS AND USES THEREOF
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:

ADDRESSEE: Rhone-Poulenc Rorer Inc.

STREET: 500 Arcola Rd. 3C43

CITY: Collegeville

STATE: PA

COUNTRY: USA

ZIP: 19426

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/612,857

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: FR 93-10971

FILING DATE: 15-SEP-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/FR94/00542

FILING DATE: 09-MAY-1994

ATTORNEY/AGENT INFORMATION:

NAME: Smith Ph.D., Julie K.

REGISTRATION NUMBER: 38,619

REFERENCE/DOCKET NUMBER: ST93044-US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (610)454-3839

TELEFAX: (610)454-3808

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 24 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid

DESCRIPTION: /desc = "oligonucleotide IV"

US-08-612-857-9

Query Match

59.0%; Score 11.8; DB 2; Length 24;

Best Local Similarity 86.7%; Pred. No. 8.2e+02;

Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 tgggttccaatcgga 18

DB 2 TCGTTTCCAAGCGA 16

RESULT 7

US-08-612-895A-29

Sequence 29, Application US/08612895A

Patent No. 5763177

GENERAL INFORMATION:

APPLICANT: GOLD, LARRY

APPLICANT: WILLIS, MICHAEL

APPLICANT: KOCH, TAD

APPLICANT: RINGQUIST, STEVEN

APPLICANT: JENSEN, KIRK

APPLICANT: ATKINSON, BRENT

TITLE OF INVENTION: SYSTEMATIC EVOLUTION OF

TITLE OF INVENTION: LIGANDS BY EXPONENTIAL

TITLE OF INVENTION: ENRICHMENT: PHOTSELECTION

TITLE OF INVENTION: OF NUCLEIC ACID LIGANDS AND

TITLE OF INVENTION: SOLUTION SELEX

NUMBER OF SEQUENCES: 64

CORRESPONDENCE ADDRESS:

ADDRESSEE: Swanson & Bratschun, L.L.C.

STREET: 8400 E. Prentice Avenue, Suite 200

CITY: Englewood

STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MG
MEDIUM TYPE: storage
COMPUTER: IBM
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/612,895A
FILING DATE: 03 August 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/10542
FILING DATE: 18 September 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/123,935
FILING DATE: 17 September 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/143,564
FILING DATE: 25 October 1993
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX10/PCT-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-612-895A-29

Query Match 59.0%; Score 11.8; DB 1; Length 35;
Best Local Similarity 40.0%; Pred. No. 8.7e+02;
Matches 6; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY 1 tgttggtttccaatc 15
:|::|::|::|::|
Db 18 UGUUUGUUCACUC 32

RESULT 8
US-09-93-293-29
Sequence 29, Application US/09093293
Patent No. 6001577
GENERAL INFORMATION:
APPLICANT: GOLD, LARRY
APPLICANT: WILLIS, MICHAEL
APPLICANT: KOCH, TAD
APPLICANT: RINGQUIST, STEVEN
APPLICANT: JENSEN, KIRK
APPLICANT: ATKINSON, BRENT
TITLE OF INVENTION: SYSTEMATIC EVOLUTION OF
LIGANDS BY EXPONENTIAL
TITLE OF INVENTION: ENRICHMENT: PHOTORESELECTION
TITLE OF INVENTION: OF NUCLEIC ACID LIGANDS AND
SOLUTION SELEX
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MG

MEDIUM TYPE: storage
COMPUTER: IBM
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 8.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/093,293
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/612,895
FILING DATE: 03 August 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/10542
FILING DATE: 18 September 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/123,935
FILING DATE: 17 September 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/143,564
FILING DATE: 25 October 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: 10 JUNE 1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: 11 JUNE 1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/931,473
FILING DATE: 17 AUGUST 1992
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX10/US-CON
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-093-293-29

Query Match 59.0%; Score 11.8; DB 3; Length 35;
Best Local Similarity 40.0%; Pred. No. 8.7e+02;
Matches 6; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY 1 tgttggtttccaatc 15
:|::|::|::|::|
Db 18 UGUUUGUUCACUC 32

RESULT 9
PCT-US94-10562A-29
Sequence 29, Application PC/TUS9410562A
GENERAL INFORMATION:
APPLICANT: GOLD, LARRY
APPLICANT: WILLIS, MICHAEL
APPLICANT: KOCH, TAD
APPLICANT: RINGQUIST, STEVEN
APPLICANT: JENSEN, KIRK
APPLICANT: ATKINSON, BRENT
TITLE OF INVENTION: SYSTEMATIC EVOLUTION OF
LIGANDS BY EXPONENTIAL
TITLE OF INVENTION: ENRICHMENT: PHOTORESELECTION
TITLE OF INVENTION: OF NUCLEIC ACID LIGANDS AND
SOLUTION SELEX
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200

CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3 1/2 inch, 1.44 MB
MEDIUM TYPE: storage
COMPUTER: IBM
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/10562A
FILING DATE: 16 SEPTEMBER 1994
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/123,935
FILING DATE: 17 September 1993
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/143,564
FILING DATE: 25 October 1993
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX10/PCT
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
PCT-US94-10562A-29

Query Match 59.0%; Score 11.8; DB 5; Length 35;
Best Local Similarity 40.0%; Pred. No. 8.7e-02;
Matches 6; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY 1 tgggtttccaatc 15
DB 18 UGUUUUUUCCACUC 32

RESULT 10
US-09-163-444-8/c
; Sequence 8, Application US/09163444
; Patent No. 6251596
; GENERAL INFORMATION:
; APPLICANT: Cook, James W.
; TITLE OF INVENTION: ASPERGILLUS N-MYRISTOYL TRANSFERASE GENES AND POLYPEPTIDES
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 07334/089001
; CURRENT APPLICATION NUMBER: US/09/163,444
; CURRENT FILING DATE: 1998-09-30
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 39
; TYPE: DNA
; ORGANISM: Aspergillus fumigatus N-myrystoyl
US-09-163-444-8

Query Match 59.0%; Score 11.8; DB 4; Length 39;
Best Local Similarity 86.7%; Pred. No. 8.8e-02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 gttggtttccaatcg 16
DB 34 GTTGTTCCTCAATAG 20

RESULT 11
US-08-765-783A-42/c
; Sequence 42, Application US/08765783A
; Patent No. 5994524
; GENERAL INFORMATION:
; APPLICANT: Matsushima, Kouji
; APPLICANT: Matsumoto, Yoshihiro
; APPLICANT: Yamada, Yoshiki
; APPLICANT: Sato, Koh
; APPLICANT: Tsuchiya, Masayuki
; APPLICANT: Yamazaki, Tatsumi
; TITLE OF INVENTION: Reshaped Human Antibody to
; INTERLEUKIN-8
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Avenue, NW, suite 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/765,783A
; FILING DATE: 07-MAR-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 35029-20001.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-887-1500
; TELEFAX: 202-822-0168
; TELEX:
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Other
; LOCATION: 1...34
; OTHER INFORMATION: L7W1 sequence
US-08-765-783A-42

Query Match 58.0%; Score 11.6; DB 2; Length 34;
Best Local Similarity 77.8%; Pred. No. 1.1e+03;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 ttgggtttccaatcgacc 20
DB 32 TTTGTTTCTTAATGAGACC 15

RESULT 12
US-08-921-100-42/c
; Sequence 42, Application US/08921100
; Patent No. 6024956
; GENERAL INFORMATION:
; APPLICANT: MATSUSHIMA, KOUJI
; APPLICANT: MATSUMOTO, YOSHIHIRO
; APPLICANT: YAMADA, YOSHIKI

APPLICANT: SATO, KOH
APPLICANT: TSUCHIYA, MASSAYUKI
APPLICANT: YAMAZAKI, TATUMI
TITLE OF INVENTION: HUMANIZED ANTI-IL8 ANTIBODY
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. NW, Suite 5500
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1888
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/921,100
FILING DATE: 29-AUG-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/437,323
FILING DATE: 09-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 15580-0001.02
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-921-100-42

Query Match 58.0%; Score 11.6; DB 3; Length 34;
Best Local Similarity 77.8%; Pred. No. 1.1e+03;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 ttggtttccaatcgacc 20
||| ||||| ||| |||||
Db 32 TTTGTTTCTAATGAGACC 15

RESULT 13
US-08-880-142-42/c
Sequence 42, Application US/08880142
Patent No. 6048972
GENERAL INFORMATION:
APPLICANT: MATSUSHIMA, KOUJI
APPLICANT: MATSUMOTO, YOSHIHIRO
APPLICANT: YAMADA, YOSHIKI
APPLICANT: SATO, KOH
APPLICANT: TSUCHIYA, MASSAYUKI
APPLICANT: YAMAZAKI, TATUMI
TITLE OF INVENTION: HUMANIZED ANTI-IL8 ANTIBODY
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. NW, Suite 5500
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1888
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/880,142
FILING DATE: 20-JUN-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/345,145
FILING DATE: 28-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 15580-0001.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-880-142-42

Query Match 58.0%; Score 11.6; DB 3; Length 34;
Best Local Similarity 77.8%; Pred. No. 1.1e+03;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 ttggtttccaatcgacc 20
||| ||||| ||| |||||
Db 32 TTTGTTTCTAATGAGACC 15

RESULT 14
US-08-902-201-42/c
Sequence 42, Application US/08902201
Patent No. 6068840
GENERAL INFORMATION:
APPLICANT: MATSUSHIMA, KOUJI
APPLICANT: MATSUMOTO, YOSHIHIRO
APPLICANT: YAMADA, YOSHIKI
APPLICANT: SATO, KOH
APPLICANT: TSUCHIYA, MASSAYUKI
APPLICANT: YAMAZAKI, TATUMI
TITLE OF INVENTION: HUMANIZED ANTI-IL8 ANTIBODY
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. NW, Suite 5500
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1888
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/902,201
FILING DATE: 29-JUL-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/437,328
FILING DATE: 09-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 15580-0001.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500

TELEFAX: (202) 887-0763
TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-902-201-42

Query Match 58.0%; Score 11.6; DB 3; Length 34;
Best Local Similarity 77.8%; Pred. No. 1.1e+03;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 ttggtttccaatcgacc 20
|| ||||| ||| ||||
Db 32 TTGTTTCTAATGAGACC 15

RESULT 15

US-09-416-557-42/c
; Sequence 42, Application US/09416557
; Patent No. 6245894
; GENERAL INFORMATION:
; APPLICANT: Matsushima, Kouji
; APPLICANT: Matsumoto, Yoshihiro
; APPLICANT: Yamada, Yoshiki
; APPLICANT: Sato, Koh
; APPLICANT: Tsuchiya, Masayuki
; APPLICANT: Yamazaki, Tatsumi
; TITLE OF INVENTION: Reshaped Human Antibody to
; INTERLEUKIN-8
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Avenue, NW, suite 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/416,557
; FILING DATE: 12-October-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/765,783
; FILING DATE: 7-March-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 35029-20001.10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-887-1500
; TELEFAX: 202-822-0168
; TELEX:
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Other
; LOCATION: 1...34
; OTHER INFORMATION: LTw1 sequence
US-09-416-557-42

Query Match 58.0%; Score 11.6; DB 4; Length 34;
Best Local Similarity 77.8%; Pred. No. 1.1e+03;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 3 ttggtttccaatcgacc 20
|| ||||| ||| ||||
Db 32 TTGTTTCTAATGAGACC 15

Search completed: October 2, 2001, 16:03:51
Job time: 14595 sec

Result No.	Query %			ID	Description
	Score	Match	Length		
1	20	100.0	20	AAC65547	Human focal adhesi
2	15	75.0	15	AAC65567	Human focal adhesi
C 3	13	65.0	19	AAQ48576	HPV E6/7 region pr
4	12.6	63.0	35	AAA12990	Cellulomonas fimi
C 5	12.6	63.0	35	AAZ54999	Neisseria species
6	12.6	63.0	43	AAQ04950	Oligonucleotide ca
7	12.4	62.0	17	AAA36501	Human genomic SNP
8	12.4	62.0	21	AAZ59639	Nucleotide sequenc
9	12.4	62.0	24	AAC66935	Arabidopsis AOX1a
10	12.2	61.0	17	AAV93672	Human B-raf substr
11	12.2	61.0	20	AAQ95843	Primer A (Group 1)

PS Claim 15; Column 23; 30pp; English.

XX The present invention describes a number of phosphorothioate antisense
CC sequences to the human focal adhesion kinase (FAK) protein. This protein
CC is involved in integrin-mediated signal transduction, and is implicated
CC in cancer, particularly colon, breast and oral tumours, embryonic
CC development disorders, angiogenic disorders and wound healing. The
CC antisense sequences, including the one shown here, can be used in the
CC treatment of all of these.

XX Sequence 20 BP; 3 A; 5 C; 5 G; 7 T; 0 other;

Query Match 100.0%; Score 20; DB 22; Length 20;

Best Local Similarity 100.0%; Pred. No. 0.16;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tgggtgttccaatcgacc 20

|||||

Db 1 tgggtgttccaatcgacc 20

RESULT 2

AAC65567

ID AAC65567 standard; DNA; 15 BP.

AC AAC65567;

XX

XX 12-FEB-2001 (first entry)

DT

DE Human focal adhesion kinase antisense sequence #33.

XX Human; focal adhesion kinase; FAK; signal transduction; cancer;

XX embryonic development disorder; angiogenic disorder; wound healing;

KW antisense; phosphorothioate; ss.

XX

OS Homo sapiens.

XX

XX US6133031-A.

XX

PD 17-OCT-2000.

XX

PF 19-AUG-1999; 99US-0377310.

XX

PR 19-AUG-1999; 99US-0377310.

XX

XX (ISIS-) ISIS PHARM INC.

PA

PI Monia BP, Gaarde WA;

XX

XX WPI; 2001-006141/01.

DR

XX

XX New antisense compounds for inhibiting focal adhesion kinase

PT expression, especially useful for inhibiting retinal

PT neovascularization, or for diagnosing and treating e.g. colon cancer -

XX

PS Example 2; Column 25; 30pp; English.

XX

XX The present invention describes a number of phosphorothioate antisense

CC sequences to the human focal adhesion kinase (FAK) protein. This protein

CC is involved in integrin-mediated signal transduction, and is implicated

CC in cancer, particularly colon, breast and oral tumours, embryonic

CC development disorders, angiogenic disorders and wound healing. The

CC antisense sequences, including the one shown here, can be used in the

CC treatment of all of these.

XX

XX Sequence 15 BP; 2 A; 3 C; 4 G; 6 T; 0 other;

Query Match

Best Local Similarity 75.0%; Score 15; DB 22; Length 15;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 ttggtttccaatcgg 17

|||||

Db 1 ttggtttccaatcgg 15

RESULT 3

AAQ48576/c

ID AAQ48576 standard; DNA; 19 BP.

XX

XX AAQ48576;

XX

XX 22-FEB-1994 (first entry)

DT

DE HPV E6/7 region probe.

XX Human papilloma virus; HPV; E6; E7; benign; malignant; probe; ss.

KW

XX Synthetic.

OS

XX JP05192200-A.

PN

XX 03-AUG-1993.

PD

XX 19-AUG-1991; 91JP-0230839.

PF

XX 20-AUG-1990; 90JP-0217067.

PR

XX (TAKI) TAKARA SHUZO CO LTD.

PA

XX WPI; 1993-277497/35.

DR

XX

XX Detecting benign and/or malignant human papilloma virus - by

PT detecting DNA sequence of E6 and/or E7 region of human papilloma

PT virus

XX

XX Disclosure; Page 17; 18pp; Japanese.

PS

XX The probe is used to detect benign and/or malignant human papilloma

CC virus. The probe binds to the E6 and/or E7 region of the virus.

CC

XX Sequence 19 BP; 7 A; 4 C; 5 G; 3 T; 0 other;

SQ

Query Match

Best Local Similarity 65.0%; Score 13; DB 14; Length 19;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tgttggtttccaa 13

|||||

Db 14 TGTGTGTTCCAA 2

RESULT 4

AAA12990

ID AAA12990 standard; DNA; 35 BP.

XX

XX AAA12990;

XX

XX 18-JUL-2000 (first entry)

DT

XX Cellulomonas fimi xylanase PCR primer, SEQ ID NO:6.

DE

XX Xylanase; endo-1,4-beta-xylanase; xylan hydrolysis;

KW xylo-oligosaccharide production; chimeric xylanase; PCR primer; ss.

XX

XX Cellulomonas fimi.

OS

XX JP3030331-B1.

PN

XX 10-APR-2000.

PD

XX 17-MAR-1999; 99JP-0071715.

PF

XX

PR 17-MAR-1999; 99JP-0071715.
XX (NORQ) NORIN-SUISANSHO SHOKUHIN SOGO KENKYUSHOCHO.
PA (SEIB-) SEIBUTSUKEI TOKUTEI SANGYO GIJUTSU KENKYU SUISHIN KIKO.
XX WPI; 2000-306509/27.
DR
XX
XX Modified xylanase gene for use in foodstuff industry, has base sequence
PT of 1065 nucleotides -
PT
XX
XX Example 1; Page 10; 11pp; Japanese.
PS
XX
XX The invention relates a novel chimeric xylanase (AA12985) and to DNA
CC encoding it (AA12985). The chimeric xylanase comprises residues 1-244
CC of Streptomyces olivaceoviridis xylanase and residues 244-354 of
CC Cellulomonas fimi xylanase. Xylanase (also known as endo-1,4-beta-
CC xylanase) hydrolyses beta-1,4-D-xylan, a component of the hemicellulose
CC in plant cell walls, into xylo-oligosaccharides and xylose. Xylanase is
CC used in a range of industrial processes. It is used to produce xylo-
CC oligosaccharides from xylan from broad-leaved trees, and is used in
CC wood- pulp bleaching to reduce the amount of chlorine required for this
CC process. Xylo-oligosaccharides can be used as ingredients in foodstuffs
CC and as water-retaining material in cosmetics. The chimeric xylanase of
CC the invention does not generate xylose monomers during the hydrolysis of
CC xylan. It is therefore useful for efficient and reliable xylo-
CC oligosaccharide production. Sequences AA12990-AA12991 represent PCR
CC primers used in an exemplification of the present invention to amplify
CC a portion of the Cellulomonas fimi xylanase gene encoding residues
CC 244-354 of the protein. The PCR product was then used to generate
CC DNA encoding the chimeric xylanase via a second round of PCR using
CC primers AA12987 and AA12991.
XX
XX
SQ Sequence 35 BP; 3 A; 15 C; 9 G; 8 T; 0 other;

Query Match 63.0%; Score 12.6; DB 21; Length 35;
Best Local Similarity 78.9%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 2 gttgtttccaatcgacc 20
||| ||||| ||| |||
Db 5 gtcggctccagtcgacc 23

RESULT 5
AAZ54999/C
ID AAZ54999 standard; DNA; 35 BP.
XX
XX
XX AAZ54999;
XX
XX 21-MAR-2000 (first entry)
XX
XX Neisseria species ORF cloning PCR primer #384.
XX
XX Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;
KW antigenic; diagnosis; immunogenic; infection; meningitis; septicaemia;
KW antibacterial; gene therapy; PCR primer; ss.
XX
XX Synthetic.
OS Neisseria sp.
XX
XX WO9957280-A2.
XX
XX 11-NOV-1999.
XX
XX 30-APR-1999; 99WO-US09346.
XX
XX 01-MAY-1998; 98US-0083758.
PR 31-JUL-1998; 98US-0094869.
PR 02-SEP-1998; 98US-0098994.
PR 02-SEP-1998; 98US-0093062.
PR 09-OCT-1998; 98US-0103749.
PR 09-OCT-1998; 98US-0103794.

PR 09-OCT-1998; 98US-0103796.
XX 25-FEB-1999; 99US-0121528.
XX
XX (CHIR) CHIRON CORP.
PA (GENO-) INST GENOMIC RES.
XX
XX Fraser C, Galeotti C, Grandi G, Hickey E, Masignani V, Mora M;
PI Petersen J, Pizza M, Rappuoli R, Ratti G, Scalato E, Scarselli M;
PI Tettelin H, Venter JC;
XX
XX WPI; 2000-062150/05.
DR
XX
XX Novel Neisserial polypeptides predicted to be useful antigens for
PT vaccines and diagnostics -
PT
XX Example 16; Page 150; 1453pp; English.
PS
XX AAZ53015 to AAZ54536, AAZ54577 to AAZ54615, and AAZ74253 to AAZ75941
CC represent novel Neisseria meningitis and N. gonorrhoea polynucleotides
CC and polypeptides. AAZ54537 to AAZ54576 and AAZ54616 to AAZ55473 represent
CC PCR primers used in the exemplification of the present invention. The
CC polypeptides, the polynucleotides, antibodies and compositions of
CC the invention can be used as vaccines, as diagnostic reagents, and as
CC immunogenic compositions. The polypeptides can be used in the
CC manufacture of medicaments for treating or preventing infection due to
CC Neisserial bacteria (e.g. meningitis and septicaemia), to detect the
CC presence of Neisseria bacteria, or to raise antibodies. They may also
CC be used to screen for agonists or antagonists, which may themselves
CC have use as antibacterial agents. The polynucleotides of the invention
CC may also be used in gene therapy protocols.
XX
XX
SQ Sequence 35 BP; 18 A; 5 C; 7 G; 5 T; 0 other;

Query Match 63.0%; Score 12.6; DB 21; Length 35;
Best Local Similarity 78.9%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 tgttggtttccaatcgacc 19
||| ||||| ||||| |||
Db 32 TGTGTGTTTTCATCAGCC 14

RESULT 6
AAQ04950
ID AAQ04950 standard; DNA; 43 BP.
XX
XX
XX AAQ04950;
XX
XX 24-OCT-1990 (first entry)
XX
XX Oligonucleotide carrying mutation for factor V gene.
XX
XX Human factor VIII analogue; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FT mutation 19..24
FT /*tag= a
XX
XX WO9005530-A.
XX
XX 31-MAY-1990.
XX
XX 14-NOV-1989; 89WO-0005049.
XX
XX 14-NOV-1988; 88US-0270882.
XX
XX (GENE-) GENETICS INST INC.
XX
XX Kaufman RJ, Pittman DD;
XX

DR WPI; 1990-193265/25.
XX New hybrid DNA encoding hybrid procoagulant proteins -
PT prep'd. by modifying DNA encoding human factor VIII.
XX
XX Disclosure; ; pp; English.
XX
XX Factor VIII analogue is sufficiently mutated from the original gene
CC that it is not recognised by blood Abs of the patient. The analogue
CC is composed of human FVIII but carries the B-domain of human FV in
CC place of the FVIII B-domain.
CC Oligonucleotides can be used to alter the profile of the blood
CC factor without significantly altering its activity.
XX
XX Sequence 43 BP; 10 A; 10 C; 11 G; 12 T; 0 other;
SQ

Query Match 63.0%; Score 12.6; DB 11; Length 43;
Best Local Similarity 78.9%; Pred. No. 1.4e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 tgttggtttccaatcgac 19
||||| ||||| |||||
Db 25 tgtaggatgccaatgggac 43

RESULT 7
AAA36501
ID AAA36501 standard; DNA; 17 BP.
XX
XX AAA36501:
AC
XX
XX 26-JUL-2000 (first entry)
DT
DE Human genomic SNP allele specific oligonucleotide SEQ ID NO:566.
XX
XX Human; single nucleotide polymorphism; SNP; genotyping; DNA analysis;
KW allele specific oligonucleotide; ASO; reduced complexity genome; RCG;
KW genomic classification; identification; DNA fingerprinting;
XX tumour characterisation; hybridisation; ss.
XX
XX Homo sapiens.
XX
XX WO200018960-A2.
PN
XX
XX 06-APR-2000.
PD
XX
XX 24-SEP-1999; 99WO-US22283.
PF
XX
XX 25-SEP-1998; 98US-0101757.
PR
XX
XX (MASI) MASSACHUSETTS INST TECHNOLOGY.
PA
XX
XX Landers JE, Jordan B, Housman DE, Charest A;
PI
XX
XX WPI; 2000-293181/25.
DR
XX
XX Detection of single nucleotide polymorphisms in genomes by preparation
PT and analysis of reduced complexity genomes, useful for genotyping,
PT fingerprinting and determining allele frequency of SNPs -
XX
XX Disclosure; Page 70; 111pp; English.
XX
XX A method has been developed for detecting the presence or absence of a
CC single nucleotide polymorphism (SNP) allele in a genomic sample. The
CC method comprises preparing a reduced complexity genome (RCG) from the
CC genomic sample and analysing the RCG for the presence or absence of a
CC SNP allele. The method can be used to characterise a tumour, to generate
CC a genomic pattern for an individual genome or to generate a genomic
CC classification code for a genome. The method can be used to assess
CC whether a subject is at risk for developing a disease or to identify a
CC set of SNP alleles associated with a disease. The method can also be
CC used to perform linkage analysis. AAA35944 to AAA35947 represent

CC sequences used in the exemplification of the present invention. AAA35948
CC to AAA36632 represent nucleotide sequences containing SNPs.
XX
XX Sequence 17 BP; 5 A; 2 C; 5 G; 5 T; 0 other;
SQ

Query Match 62.0%; Score 12.4; DB 21; Length 17;
Best Local Similarity 92.9%; Pred. No. 1.6e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 5 ggtttccaatcgga 18
||||| ||||| |||||
Db 1 ggtttccaatggga 14

RESULT 8
AAZ99639
ID AAZ99639 standard; DNA; 21 BP.
XX
XX AAZ99639:
AC
XX
XX 12-JUL-2000 (first entry)
DT
DE Nucleotide sequence of G-motif oligonucleotide P2314.
XX
XX G-motif oligonucleotide; vaccine; Toxoplasmosis; viral infection;
KW antigen presenting cell activation; natural killer cell; septic shock;
KW cytotoxic T-lymphocyte; inflammation; autoimmune disease;
KW rheumatoid arthritis; Crohn's disease; sarcoidosis; multiple sclerosis;
KW Kawasaki syndrome; graft-versus-host disease; transplant rejection;
KW helper T cell response 1-mediated disease; Lyme arthritis;
KW Streptococcal induced arthritis; chronic inflammatory bowel disease;
KW psoriasis vulgaris; experimental allergic encephalomyelitis;
KW insulin-dependent diabetes mellitus; bacterial infection;
KW parasitic infection; Leishmaniasis; spontaneous abortion; tumour; ss.
XX
XX Synthetic.
OS
XX
XX WO200014217-A2.
PN
XX
XX 16-MAR-2000.
PD
XX
XX 03-SEP-1999; 99WO-EP06502.
PF
XX
XX 03-SEP-1998; 98EP-0116852.
PR
XX
XX (CPGI-) CPG IMMUNOPHARMACEUTICALS GMBH.
PA
XX
XX Wagner H, Lipford GB, Heeg K;
PI
XX
XX WPI; 2000-256970/22.
DR
XX
XX Compositions comprising G-motif oligonucleotides useful for treating
PT e.g. septic shock, rheumatoid arthritis, diabetes and human
PT immunodeficiency virus infections -
XX
XX Disclosure; Page 34; 75pp; English.
XX
XX The present sequence represents a G-motif oligonucleotide of the
CC invention. The specification describes compositions comprising G-motif
CC oligonucleotides. The G-motif oligonucleotides inhibit activation of
CC antigen presenting cells by inhibiting the uptake of DNA by a cell, by
CC stimulating natural killer cells, or by co-stimulating cytotoxic
CC T-lymphocytes. The G-motif oligonucleotides may be used for the
CC production of vaccines for treating septic shock, inflammation,
CC autoimmune diseases (e.g. rheumatoid arthritis, Crohn's disease,
CC sarcoidosis, multiple sclerosis, Kawasaki syndrome, graft-versus-host
CC disease and transplant rejection), helper T cell response 1-mediated
CC diseases (e.g. Streptococcal induced arthritis, Lyme arthritis, chronic
CC inflammatory bowel disease, psoriasis vulgaris, experimental allergic
CC encephalomyelitis, and insulin-dependent diabetes mellitus), bacterial
CC infections, parasitic infections (e.g. Leishmaniasis or Toxoplasmosis),
CC viral infections (e.g. Cytomegalovirus and human immunodeficiency virus

CC (HIV)-infections), spontaneous abortions and tumours. They may also be
 CC used to induce proliferation of bone marrow cells, especially macrophage
 CC precursor cells.

XX Sequence 21 BP; 2 A; 5 C; 3 G; 11 T; 0 other;

Query Match 62.0%; Score 12.4; DB 21; Length 21;
 Best Local Similarity 92.9%; Pred. No. 1.6e+03;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tgggtgttcacat 14
 |||||
 Db 8 tgggtgttcacat 21

RESULT 9

AAC66935
 ID AAC66935 standard; DNA; 24 BP.

XX
 AC AAC66935;

XX 27-MAR-2001 (first entry)

XX Arabidopsis AOXla gene promoter PCR primer #2.

XX Plant signal transduction pathway; reporter vector;

KW luciferase; herbicide resistance; pest resistance; PCR primer; ss.

XX Arabidopsis thaliana.

XX WO200071668-A2.

XX 30-NOV-2000.

XX 22-MAY-2000; 2000WO-US14041.

XX 20-MAY-1999; 99US-0136145.

XX (UYNE-) UNIV NEBRASKA.

XX Rhoades DM;

XX WPI; 2001-025143/03.

XX Identifying genes encoding signal transduction components useful for
 PT producing transgenic plants, by transforming plants with vector
 PT encoding reporter gene, mutating the plant and identifying genes from
 PT the mutant

XX Example 1; Page 54; 54pp; English.

XX The present invention provides a method for identifying genes encoding
 CC components of plant signal transduction pathways between mitochondrial
 CC function and metabolic status and nuclear gene expression. This involves
 CC the transformation of a plant with a vector encoding a reporter gene
 CC linked to an AOX promoter, mutagenesis of the plant to increase
 CC expression of the reporter gene and then determining the identity of the
 CC signal transduction gene of interest. This is useful in the production of
 CC transgenic plants with increased productivity, herbicide, stress and pest
 CC resistance.

XX Sequence 24 BP; 6 A; 5 C; 5 G; 8 T; 0 other;

Query Match 62.0%; Score 12.4; DB 22; Length 24;
 Best Local Similarity 92.9%; Pred. No. 1.6e+03;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 tgggttcacatcg 17

Db 11 tgggttcacatcg 24

RESULT 10

AAV93672

ID AAV93672 standard; RNA; 17 BP.

XX
 AC AAV93672;

XX 18-FEB-1999 (first entry)

XX Human B-raf substrate nucleotide position 2272.

XX Human; c-raf; A-raf; B-raf; hammerhead ribozyme; hairpin ribozyme;
 KW target; substrate; catalyst; modulation; expression; Raf gene;
 KW delivery; screening; identification; synthesis; deprotection;
 KW purification; cancer; inflammation; psoriasis; non-hepatic ascites;
 KW infection; genetic drift; restenosis; rheumatoid arthritis; ss.

XX Homo sapiens.

XX WO9850530-A2.

XX 12-NOV-1998.

XX 05-MAY-1998; 98WO-US09249.

XX 19-DEC-1997; 97US-0068212.

XX 09-MAY-1997; 97US-0046059.

XX 09-JUN-1997; 97US-0049002.

XX 03-JUL-1997; 97US-0051718.

XX 22-AUG-1997; 97US-0056808.

XX 02-OCT-1997; 97US-0061321.

XX 02-OCT-1997; 97US-0061324.

XX 05-NOV-1997; 97US-0064866.

XX (RIBO-) RIBOZYME PHARM INC.

XX Beaudry A, Beigelman L, Bellon L, Burgin A, Jarvis T;

XX Karpeisky A, Kisich K, Matulic-Adamic J, McSwigen JA;

XX Parry T, Reynolds M, Sweedler D, Thompson J, Workman CT;

XX WPI; 1999-009494/01.

XX Identifying new catalytic nucleic acid that modulates selected

XX processes - especially ribozymes that cleave Raf RNA for treating

XX cancer, restenosis, and also new ribozymes and modified nucleoside

XX triphosphates used as antiviral agents and synthons

XX Claim 177; Page 172; 259pp; English.

XX A method has been developed for the identification of a nucleic acid
 CC capable of modulating a process in a biological system. The method
 CC comprises: (a) introducing into the system a random library of nucleic
 CC acid catalysts (NAC) having a substrate binding domain (SBD), comprising
 CC a random sequence, and a catalytic domain (CD); and (b) identifying NAC
 CC in systems where modulation has occurred and/or determining the sequence
 CC of at least part of the SBDs in such systems. Nucleic acid molecules
 CC with endonuclease activity and catalytic activity, from the present
 CC invention, are used to modulate gene expression in plant and mammalian
 CC cells and to cleave target nucleic acid, particularly for treating
 CC systemic diseases caused by specific RNA, e.g. cancer, inflammation,
 CC psoriasis, non-hepatic ascites and infection. They may also be used to
 CC detect genetic drift and mutations in diseased cells and to determine
 CC c-raf RNA. Specifically NACs with RNA-cleaving activity that modulate
 CC expression of the Raf gene, are used to treat cancer, restenosis,
 CC psoriasis or rheumatoid arthritis, or generally any condition associated
 CC with the level of c-raf. Introduction of sugar/phosphate modifications
 CC increases stability against nuclease and activity. AAV90922 to AAV93877
 CC represent NACs that can be used in the method, specifically for
 CC modulating the expression of a Raf gene.

XX Sequence 17 BP; 5 A; 4 C; 4 G; 4 U; 0 other;

Query Match 61.0%; Score 12.2; DB 20; Length 17;
 Best Local Similarity 58.8%; Pred. No. 2e+03;
 Matches 10; Conservative 4; Mismatches 0; Gaps 0;

QY 2 gttggtttccaatcgga 18
 | :|||:||||| |
 Db 1 gcugguuuccaacaag 17

RESULT 11

AAQ95843
 ID AAO95843 standard; DNA; 20 BP.

XX AC AAO95843;

XX DT 21-FEB-1996 (first entry)

XX DE Primer A (Group 11, set A) for marker D9S180, chromosome 9.

XX KW primer; polymerase chain reaction; PCR; linkage study; locus;
 KW microsatellite marker sequence; automated genotyping; allele;
 KW polymorphism; detection; Homo sapiens; ss.

XX OS Synthetic.

XX PN WO9515400-AL.

XX PD 08-JUN-1995.

XX PF 05-DEC-1994; 94WO-US13945.

XX PR 03-DEC-1993; 93US-0160837.

XX PA (UYJO) UNIV JOHNS HOPKINS.

XX PI Levitt RC;

XX DR WPI; 1995-215278/28.

XX PT Kit for automated genotyping contg. pairs of PCR primers - designed
 PT to amplify polymorphic nucleotide repeat sequences, arranged in sets
 PT each with a characteristic fluorescence label, useful e.g. in
 PT detection of disease related genetic rearrangement

XX PS Disclosure; Fig 7K-2; 104pp; English.

XX CC The method aims to provide a collection of highly reproducible
 CC microsatellite marker sequences (MMS) at approx. 10-50 cm intervals
 CC throughout the human genome which can be detectably labelled. The
 CC MMS are polymorphic, simple sequence repeats and can be used in
 CC automated genotyping. esp. fluorescence-based. The primers correspond
 CC to the unique DNA sequence surrounding each marker, and PCR is used to
 CC detect each polymorphism. When the MMS show considerable polymorphism
 CC (ie. a difference in the number of repeats) between individuals, the
 CC markers can be particularly informative. The MMS can be ideal for
 CC linkage studies. Kits comprise at least 4 groups, of at least 3 sets,
 CC each comprising labelled primers for PCR amplification of the DNA.
 CC Group 11 primer pairs are shown in AAO95841-82. The published size range
 CC of the D9S180 allele is 220-265 bp, and the degree of heterozygosity
 CC in the population is about 63%.

XX SQ Sequence 20 BP; 5 A; 4 C; 6 G; 5 T; 0 other;

Query Match 61.0%; Score 12.2; DB 16; Length 20;
 Best Local Similarity 82.4%; Pred. No. 2e+03;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 tgggtttccaatcggaac 20
 | ||||| ||||| ||
 Db 4 tgggttggaaatcgacc 20

RESULT 12
 AAV23724/c
 ID AAV23724 standard; DNA; 28 BP.

XX AC AAV23724;

XX DT 20-AUG-1998 (first entry)

XX DE PCR primer used in the course of the invention.

XX KW Lipase; variant; improved wash performance; removal; lipid stain;
 KW reduced calcium dependence; one-cycle wash efficiency; detergent;
 KW cleaning composition; PCR primer; ss.

XX OS Synthetic.

XX OS Pseudomonas pseudoalcaligenes.

XX PN WO9808939-AL.

XX PD 05-MAR-1998.

XX PF 26-AUG-1997; 97WO-DK00345.

XX PR 29-AUG-1996; 96US-0029190.

XX PR 27-AUG-1996; 96DK-0000902.

XX PA (NOVO) NOVO-NORDISK AS.

XX PI Okkels JS, Svendsen A;

XX DR WPI; 1998-230259/20.

XX PT Variants of lipase from Pseudomonas containing specific amino acid
 PT substitutions - deletions or additions, having improved wash
 PT performance in detergent formulations

XX PS Disclosure; Page 75; 104pp; English.

XX CC PCR primers AAV23717-32 were used during the course of the invention.
 CC The specification describes Pseudomonas pseudoalcaligenes lipase
 CC variants. The variant lipases described in the specification has have
 CC better wash performance than the original lipase. It has improved
 CC removal of lipid stains, reduced calcium dependence, better compatibility
 CC with detergents or their components, increased hydrophobicity, altered
 CC substrate specificity and better one-cycle wash efficiency. The variant
 CC lipase is used in detergent and cleaning compositions.

XX SQ Sequence 28 BP; 7 A; 7 C; 8 G; 6 T; 0 other;

Query Match 61.0%; Score 12.2; DB 19; Length 28;
 Best Local Similarity 82.4%; Pred. No. 2.1e+03;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 ttggtttccaatcggaac 19
 | ||||| || ||
 Db 21 TTGGTTTCGAACCGAAC 5

RESULT 13

AAAX21962/c
 ID AAX21962 standard; DNA; 32 BP.

XX AC AAX21962;

XX DT 18-MAY-1999 (first entry)

XX DE Primer BB10 for human growth hormone gene.

XX KW PCR primer; human; growth hormone; variant; cachexia; erythropoietin;
 KW erythrocyte formation; interferon; antiviral; antitumour; interleukin;
 KW immunomodulatory agent; colony-stimulating factor;
 KW proliferation stimulation; ss.

XX Synthetic.
OS Homo sapiens.
XX
PN WO9903887-A1.
XX
PD 28-JAN-1999.
XX
XX 13-JUL-1998; 98WO-US14497.
PF
XX 14-JUL-1997; 97US-0052516.
PR
PA (BOLD-) BOLDER BIOTECHNOLOGY INC.
XX
XX Cox GN;
PI
XX WPI; 1999-132163/11.
DR
XX
XX New variants of growth hormone superfamily proteins containing an
PT extra cysteine - useful, e.g. for treatment of short stature or
PT cachexia, to stimulate erythrocyte formation and as immunomodulator
XX
PS Example 1; Page 16; 94pp; English.
XX
CC This sequence is a PCR primer for the human growth hormone gene. The
CC invention relates to a variant of a member of the growth hormone (GH)
CC superfamily that has a Cys residue: (a) replacing an amino acid (aa) in
CC the loop regions, near the end of the alpha-helices or in front of, or
CC after, the first amphipathic helix; (b) added to the N- or C- terminus;
CC or (c) introduced between two aa in the loop region, at the ends of the
CC alpha-helices or in front of, or after, the first amphipathic helix. The
CC variants are used for the same therapeutic purposes as the wild type
CC sequences, e.g. for GH to treat short stature or cachexia; for
CC erythropoietin (EPO) to stimulate erythrocyte formation; for interferons
CC as antiviral, antitumour or immunomodulatory agents; for
CC colony-stimulating factors or interleukins for stimulating proliferation,
CC differentiation and function of particular types of (haematopoietic)
CC cells. Incorporation of Cys at a non-essential position allows
CC site-specific attachment of e.g. poly(ethylene glycol) (PEG) to create a
CC conjugate with increased circulation time in vivo. This reduces the need
CC for frequent injections and the cost of treatment. Modification with PEG
CC also increases solubility and stability of the protein and reduces its
CC immunogenicity.
XX
SQ Sequence 32 BP; 7 A; 13 C; 6 G; 6 T; 0 other;

Query Match 61.0%; Score 12.2; DB 20; Length 32;
Best Local Similarity 82.4%; Pred. No. 2.1e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 tgggttcacatcgacc 20
||| ||| ||||| |
Db 21 TGGATTCTAATCGGATC 5

RESULT 14
AAA74774/c
ID AAA74774 standard; DNA; 32 BP.
XX
AC AAA74774;
XX
DT 17-JAN-2001 (first entry)
XX
DE E. coli stII signal sequence PCR primer BB10.
XX
XX Erythropoietin; growth hormone; IFN-alpha2; free cysteine residue;
KW PCR primer; ss.
XX
OS Escherichia coli.
XX
PN WO200042175-A1.
XX

PD 20-JUL-2000.
XX
XX 14-JAN-2000; 2000WO-US00931.
PF
XX 14-JAN-1999; 99US-0116041.
PR
XX (BOLD-) BOLDER BIOTECHNOLOGY INC.
PA
XX Cox GN, Doherty DH, Rosendahl MS;
PI
XX WPI; 2000-476056/41.
DR
XX
XX Producing a soluble protein having a free cysteine comprises exposing a
PT host cell expressing the soluble protein to a cysteine blocking agent,
PT useful for producing recombinant human growth factor and erythropoietin
PT .
XX
PS Example 2; Page 18; 86pp; English.
XX
XX The present invention concerns novel methods of producing proteins with
CC free cysteine residues. The PCR primers AAA74770-A74854 were used to
CC amplify sequences encoding the human growth hormone, erythropoietin and
CC IFN-alpha2 proteins, and signal sequences used to control their
CC secretion, and change these sequences in order to alter their efficacy.
CC One example of modifications is the addition of polyethylene glycol
CC moieties. The proteins could then be produced in cell cultures and
CC isolated for use in the treatment of disorders such as those associated
CC with growth hormone, erythropoietin or IFN-alpha2.
XX
SQ Sequence 32 BP; 7 A; 13 C; 6 G; 6 T; 0 other;

Query Match 61.0%; Score 12.2; DB 21; Length 32;
Best Local Similarity 82.4%; Pred. No. 2.1e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 tgggttcacatcgacc 20
||| ||| ||||| |
Db 21 TGGATTCTAATCGGATC 5

RESULT 15
AAA74783/c
ID AAA74783 standard; DNA; 34 BP.
XX
AC AAA74783;
XX
DT 17-JAN-2001 (first entry)
XX
DE Human growth hormone mutagenic primer BB33.
XX
XX Erythropoietin; growth hormone; IFN-alpha2; free cysteine residue;
KW PCR primer; ss.
XX
OS Homo sapiens.
XX
XX WO200042175-A1.
PN
PD 20-JUL-2000.
XX
XX 14-JAN-2000; 2000WO-US00931.
PF
XX 14-JAN-1999; 99US-0116041.
PR
XX (BOLD-) BOLDER BIOTECHNOLOGY INC.
PA
XX Cox GN, Doherty DH, Rosendahl MS;
PI
XX WPI; 2000-476056/41.
DR
XX
XX Producing a soluble protein having a free cysteine comprises exposing a
PT host cell expressing the soluble protein to a cysteine blocking agent,
PT useful for producing recombinant human growth factor and erythropoietin
PT .

PT
XX

PS Example 4; Page 24; 86pp; English.

XX

CC The present invention concerns novel methods of producing proteins with
CC free cysteine residues. The PCR primers AAA74770-A74854 were used to
CC amplify sequences encoding the human growth hormone, erythropoietin and
CC IFN-alpha2 proteins, and signal sequences used to control their
CC secretion, and change these sequences in order to alter their efficacy.
CC One example of modifications is the addition of polyethylene glycol
CC moieties. The proteins could then be produced in cell cultures and
CC isolated for use in the treatment of disorders such as those associated
CC with growth hormone, erythropoietin or IFN-alpha2.

XX

SQ Sequence 34 BP; 8 A; 11 C; 9 G; 6 T; 0 other;

Query Match

Best Local Similarity 61.08; Score 12.2; DB 21; Length 34;

Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 4 tggtttccaatcgacc 20

||| ||| ||||| |

Db 29 TGGATTCTATCGGATC 13

Search completed: October 2, 2001, 16:18:43
Job time: 15487 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 2, 2001, 16:03:49 ; Search time 417.38 Seconds
(without alignments)
9.071 Million cell updates/sec

Title: US-09-757-100B-12

Perfect score: 20

Sequence: 1 cctgacatcagtagcatctc 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 324599 seqs, 9465562 residues

Total number of hits satisfying chosen parameters: 460742

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA.*

- 1: /cgn2_6/ptodata/1/ina/5A_COMB.seq.*
- 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*
- 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*
- 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*
- 5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq.*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	20	100.0	20	3	US-09-377-310-12
2	15	75.0	15	3	US-09-377-310-32
C 3	13.8	69.0	17	1	US-08-373-124A-1431
C 4	13.8	69.0	17	1	US-08-435-628-1431
C 5	13.8	69.0	30	1	US-08-235-503B-64
C 6	13.8	69.0	30	5	PCT-US95-05265-64
C 7	13.6	68.0	42	1	US-07-834-539A-12
C 8	13.6	68.0	42	1	US-08-053-131-64
C 9	13.6	68.0	42	1	US-08-645-641-64
C 10	13.6	68.0	42	1	US-07-853-408B-64
C 11	13.6	68.0	42	1	US-08-096-762-64
C 12	13.6	68.0	42	2	US-08-800-353-12
C 13	13.6	68.0	42	2	US-08-308-865-64
C 14	13.6	68.0	42	4	US-09-042-353-188
C 15	13.6	68.0	42	4	US-09-042-353-225
C 16	13.6	68.0	42	5	PCT-US92-06185-12
C 17	13.6	68.0	42	5	PCT-US92-10993-64
C 18	13.2	66.0	30	1	US-07-832-905B-17
C 19	13.2	66.0	30	2	US-08-700-757-17
C 20	13	65.0	23	1	US-08-464-531-59
C 21	13	65.0	23	2	US-08-461-598-59
C 22	13	65.0	23	3	US-08-322-137-59
C 23	13	65.0	36	2	US-08-585-684B-937
C 24	13	65.0	36	4	US-09-038-073-937
C 25	12.8	64.0	21	1	US-08-368-803-20
C 26	12.8	64.0	21	2	US-08-578-096A-21
C 27	12.8	64.0	21	3	US-08-790-517-11
					Sequence 12, Appl
					Sequence 32, Appl
					Sequence 1431, Ap
					Sequence 1431, Ap
					Sequence 64, Appl
					Sequence 64, Appl
					Sequence 12, Appl
					Sequence 64, Appl
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					Sequence 12, Appl
					Sequence 64, Appl
					Sequence 12, Appl
					Sequence 64, Appl
					Sequence 12, Appl
					Sequence 17, Appl
					Sequence 59, Appl
					Sequence 59, Appl
					Sequence 59, Appl
					Sequence 937, App
					Sequence 937, App
					Sequence 20, Appl
					Sequence 21, Appl
					Sequence 11, Appl

ALIGNMENTS

RESULT 1

US-09-377-310-12
; Sequence 12, Application US/09377310B
; Patent No. 6133031
; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P.
; APPLICANT: Gaarde, William A.
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
; FILE REFERENCE: ISPH-0389
; CURRENT APPLICATION NUMBER: US/09/377,310B
; CURRENT FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
US-09-377-310-12

Query Match 100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.046;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cctgacatcagtagcatctc 20
Db 1 cctgacatcagtagcatctc 20

RESULT 2

US-09-377-310-32
; Sequence 32, Application US/09377310B
; Patent No. 6133031
; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P.
; APPLICANT: Gaarde, William A.
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
; FILE REFERENCE: ISPH-0389
; CURRENT APPLICATION NUMBER: US/09/377,310B
; CURRENT FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 32
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence

Sequence 21, Appl
Sequence 17, Appl
Sequence 20, Appl
Sequence 20, Appl
Sequence 20, Appl
Sequence 2219, Ap
Sequence 2219, Ap
Sequence 2004, Ap
Sequence 2004, Ap
Sequence 2091, Ap
Sequence 2091, Ap
Sequence 9, Appl
Sequence 24, Appl
Sequence 20, Appl
Sequence 20, Appl
Sequence 19, Appl
Sequence 19, Appl
Sequence 1327, Ap

; FEATURE:
; OTHER INFORMATION: antisense sequence
US-09-377-310-32

Query Match 75.0%; Score 15; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 tgacatcagtagcat 17
Db 1 tgacatcagtagcat 15

RESULT 3

US-08-373-124A-1431/c
; Sequence 1431, Application US/08373124A
; Patent No. 5646042
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Draper, Kenneth
; APPLICANT: McSwiggen, James
; APPLICANT: Jarvis, Thale
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
; TITLE OF INVENTION: CANCER USING RIBOZYMES
; NUMBER OF SEQUENCES: 2627
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071

COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/373,124A
; FILING DATE: January 13, 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/245,466
; FILING DATE: May 18, 1994
; APPLICATION NUMBER: 08/192,943
; FILING DATE: February 7, 1994
; APPLICATION NUMBER: 07/987,132
; FILING DATE: December 7, 1992
; APPLICATION NUMBER: 07/936,422
; FILING DATE: August 26, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 209/035
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1431:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-373-124A-1431

Query Match 69.0%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 79;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 gacatcagtagcatctc 20
Db 17 GACATCAGGAGCAACTC 1

RESULT 4

US-08-435-628-1431/c
; Sequence 1431, Application US/08435628
; Patent No. 5817796
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Draper, Kenneth
; APPLICANT: McSwiggen, James
; APPLICANT: Jarvis, Thale
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
; TITLE OF INVENTION: CANCER USING RIBOZYMES
; NUMBER OF SEQUENCES: 2627
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071

COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,628
; FILING DATE: 05-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/373,124
; FILING DATE: January 13, 1995
; APPLICATION NUMBER: 08/245,466
; FILING DATE: May 18, 1994
; APPLICATION NUMBER: 08/192,943
; FILING DATE: February 7, 1994
; APPLICATION NUMBER: 07/987,132
; FILING DATE: December 7, 1992
; APPLICATION NUMBER: 07/936,422
; FILING DATE: August 26, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 209/035
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1431:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-435-628-1431

Query Match 69.0%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 79;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 gacatcagtagcatctc 20
Db 17 GACATCAGGAGCAACTC 1

```
RESULT 5
PCT-US95-503B-64/c
; Sequence 64, Application US/08235503B
; Patent No. 5563036
; GENERAL INFORMATION:
; APPLICANT: Peterson, Michael G
; APPLICANT: Balchwal, Vijay R
; APPLICANT: Strulovici, Berta
; TITLE OF INVENTION: TRANSCRIPTION FACTOR-DNA ASSAY
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/235,503B
; FILING DATE: 29-APR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman, Richard A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: A-59332/RAO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 64:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-235-503B-64

Query Match 69.0%; Score 13.8; DB 1; Length 30;
Best Local Similarity 88.2%; Pred. No. 88;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 cctgacatcagtagcat 17
Db 27 CCTGATATCATTAGCAT 11

RESULT 6
PCT-US95-05265-64/c
; Sequence 64, Application PC/TUS9505265
; GENERAL INFORMATION:
; APPLICANT: TULARIK, INC.
; TITLE OF INVENTION: TRANSCRIPTION FACTOR-DNA BINDING ASSAY
; NUMBER OF SEQUENCES: 74
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/834,539A
; FILING DATE: 1992-02-05
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 14643-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-543-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 42 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/05265
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/235,503
; FILING DATE: 29-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman, Richard A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: FP-59232-PC/RAO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 64:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; PCT-US95-05265-64

Query Match 69.0%; Score 13.8; DB 5; Length 30;
Best Local Similarity 88.2%; Pred. No. 88;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 cctgacatcagtagcat 17
Db 27 CCTGATATCATTAGCAT 11

RESULT 7
US-07-834-539A-12/c
; Sequence 12, Application US/07834539A
; GENERAL INFORMATION:
; APPLICANT: Lonberg, Nils
; APPLICANT: Kay, Robert M.
; TITLE OF INVENTION: Transgenic Non-Human Animals Capable of
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: William M. Smith
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/834,539A
; FILING DATE: 1992-02-05
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 14643-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-543-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 42 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
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US-07-834-539A-12

Query Match 68.0%; Score 13.6; DB 1; Length 42;
Best Local Similarity 80.0%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 cctgacatcagtagcatctc 20
|| ||||| ||||| |
Db 35 CCAGACATCAAAAGCATCAC 16

RESULT 8

US-08-053-131-64/c
; Sequence 64, Application US/08053131
; Patent No. 5661016
; GENERAL INFORMATION:
; APPLICANT: Lonberg, Nils
; APPLICANT: Kay, Robert M.
; TITLE OF INVENTION: Transgenic No. 5661016-Human Animals for
; TITLE OF INVENTION: Producing Heterologous Antibodies
; NUMBER OF SEQUENCES: 197
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 200
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/053,131
; FILING DATE: 26-APR-1993
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/990,860
; FILING DATE: 16-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/810,279
; FILING DATE: 17-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/853,408
; FILING DATE: 18-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 14643-9-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 64:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 42 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (primer)
; US-08-053-131-64

Query Match 68.0%; Score 13.6; DB 1; Length 42;
Best Local Similarity 80.0%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 cctgacatcagtagcatctc 20
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Db 35 CCAGACATCAAAAGCATCAC 16

RESULT 9

US-08-645-641-64/c
; Sequence 64, Application US/08645641
; Patent No. 5719032
; GENERAL INFORMATION:
; APPLICANT: Lonberg, Nils
; APPLICANT: Kay, Robert M.
; TITLE OF INVENTION: Transgenic No. 5719032-Human Animals for
; TITLE OF INVENTION: Producing Heterologous Antibodies
; NUMBER OF SEQUENCES: 150
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: William M. Smith
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/645,641
; FILING DATE: 20-MAY-1996
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/904,068
; FILING DATE: 23-JUN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 14643-000913
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 64:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 42 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (primer)
; US-08-645-641-64

Query Match 68.0%; Score 13.6; DB 1; Length 42;
Best Local Similarity 80.0%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 cctgacatcagtagcatctc 20
|| ||||| ||||| |
Db 35 CCAGACATCAAAAGCATCAC 16

RESULT 10

US-07-853-408B-64/c
; Sequence 64, Application US/07853408B
; Patent No. 5789650
; GENERAL INFORMATION:
; APPLICANT: Lonberg, Nils
; APPLICANT: Kay, Robert M.
; TITLE OF INVENTION: Transgenic No. 5789650-Human Animals for
; TITLE OF INVENTION: Producing Heterologous Antibodies
; NUMBER OF SEQUENCES: 150
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: William M. Smith
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 19920318
; APPLICATION NUMBER: US/07/853.408B
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 14643-9
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 64:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 42 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (primer)
; US-07-853-408B-64

Query Match 68.0%; Score 13.6; DB 1; Length 42;
Best Local Similarity 80.0%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 cctgacatcagtagcatctc 20
|| ||||| ||||| |
Db 35 CCAGACATCAAAAGCATCAC 16

RESULT 11

US-08-096-762-64/c
; Sequence 64, Application US/08096762
; Patent No. 5814318
; GENERAL INFORMATION:
; APPLICANT: Lonberg, Nils
; TITLE OF INVENTION: Transgenic No. 5814318-Human Animals for
; TITLE OF INVENTION: Producing Heterologous Antibodies
; NUMBER OF SEQUENCES: 210
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 200
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/096,762
; FILING DATE: 22-JUL-1993
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/053,131
; FILING DATE: 26-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/990,860
; FILING DATE: 16-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/904,068
; FILING DATE: 23-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/853,408
; FILING DATE: 18-MAR-1992
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/810,279
; FILING DATE: 17-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 14643-9-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 64:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 42 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (primer)
; US-08-096-762-64

Query Match 68.0%; Score 13.6; DB 1; Length 42;
Best Local Similarity 80.0%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 cctgacatcagtagcatctc 20
|| ||||| ||||| |
Db 35 CCAGACATCAAAAGCATCAC 16

RESULT 12

US-08-800-353-12/c
; Sequence 12, Application US/08800353
; Patent No. 5874299
; GENERAL INFORMATION:
; APPLICANT: Lonberg, Nils
; TITLE OF INVENTION: Transgenic No. 5874299-Human Animals Capable of
; TITLE OF INVENTION: Producing Heterologous Antibodies
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: William M. Smith
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/800,353
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/834,539
; FILING DATE: 1992-02-05
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 14643-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-543-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 42 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-800-353-12

Query Match 68.0%; Score 13.6; DB 2; Length 42;
Best Local Similarity 80.0%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 cctgacatcagtagcatctc 20
|| ||||| ||||| |
Db 35 CCAGACATCAAAAGCATCAC 16

RESULT 13

US-08-308-865-64/c
; Sequence 64, Application US/08308865
; Patent No. 5877397
; GENERAL INFORMATION:
; APPLICANT: Lonberg, Nils
; APPLICANT: Kay, Robert M.
; TITLE OF INVENTION: Transgenic No. 5877397-Human Animals for
; TITLE OF INVENTION: Producing Heterologous Antibodies
; NUMBER OF SEQUENCES: 150
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: William M. Smith
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/308,865
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/145,707
; FILING DATE:
; APPLICATION NUMBER: US/07/904,068
; FILING DATE: 23-JUN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 14643-9-1-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 64:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 42 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (primer)
US-08-308-865-64

Query Match 68.0%; Score 13.6; DB 2; Length 42;
Best Local Similarity 80.0%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 cctgacatcagtagcatctc 20
|| ||||| ||||| |
Db 35 CCAGACATCAAAAGCATCAC 16

RESULT 14

US-09-042-353-188/c
; Sequence 188, Application US/09042353
; Patent No. 6255458
; GENERAL INFORMATION:
; APPLICANT: Lonberg, Nils

APPLICANT: Kay, Robert M.
; TITLE OF INVENTION: Transgenic No. 6255458-Human Animals for
; TITLE OF INVENTION: Producing Heterologous Antibodies
; NUMBER OF SEQUENCES: 421
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/042,353
; FILING DATE: 13-MAR-1998
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/810,279
; FILING DATE: 17-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/853,408
; FILING DATE: 18-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/904,068
; FILING DATE: 23-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/990,860
; FILING DATE: 16-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/053,131
; FILING DATE: 26-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/096,762
; FILING DATE: 22-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/155,301
; FILING DATE: 18-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/161,739
; FILING DATE: 03-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/165,699
; FILING DATE: 10-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/209,741
; FILING DATE: 09-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/352,322
; FILING DATE: 07-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/544,404
; FILING DATE: 10-OCT-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/728,463
; FILING DATE: 10-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US96/16433
; FILING DATE: 10-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/758,417
; FILING DATE: 02-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/21803
; FILING DATE: 01-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 014643-009040US
; TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 188:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-09-042-353-188

Query Match 68.0%; Score 13.6; DB 4; Length 42;
Best Local Similarity 80.0%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 cctgacatcagtagcatctc 20
|| ||||| ||||| I
Db 35 CCAGACATCAAAAGCATCAC 16

RESULT 15
US-09-042-353-225/C
Sequence 225, Application US/09042353
Patent No. 6255458
GENERAL INFORMATION:
APPLICANT: Lonberg, Nils
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 6255458-Human Animals for
TITLE OF INVENTION: Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 421
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/042,353
FILING DATE: 13-MAR-1998
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/810,279
FILING DATE: 17-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/853,408
FILING DATE: 18-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/904,068
FILING DATE: 23-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/053,131
FILING DATE: 26-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/096,762
FILING DATE: 22-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/155,301
FILING DATE: 18-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/161,739
FILING DATE: 03-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/165,699

FILING DATE: 10-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/209,741
FILING DATE: 09-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/352,322
FILING DATE: 07-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/544,404
FILING DATE: 10-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/728,463
FILING DATE: 10-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US96/16433
FILING DATE: 10-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/758,417
FILING DATE: 02-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/21803
FILING DATE: 01-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 014643-009040US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 225:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-09-042-353-225

Query Match 68.0%; Score 13.6; DB 4; Length 42;
Best Local Similarity 80.0%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 cctgacatcagtagcatctc 20
|| ||||| ||||| I
Db 35 CCAGACATCAAAAGCATCAC 16

Search completed: October 2, 2001, 16:03:50
Job time: 14594 sec

MOLECULE TYPE: DNA (genomic)
US-08-466-588-52

Query Match 76.0%; Score 15.2; DB 8; Length 40;
Best Local Similarity 85.0%; Pred. No. 6.1e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 attctcgtcgtcgtgtaa 20
||||| ||| |||
DB 21 ATTCTCGTGTGCGCGAA 2

RESULT 5

US-09-377-310-37
Sequence 37, Application PC/TUS0018999
GENERAL INFORMATION:
APPLICANT: Isis Pharmaceuticals, Inc.
APPLICANT: Monia, Brett P.
APPLICANT: Gaarde, William A.
APPLICANT: Nero, Pamela S.
TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
FILE REFERENCE: ISPH-0476
CURRENT APPLICATION NUMBER: PCT/US00/18999
CURRENT FILING DATE: 2000-07-13
PRIOR APPLICATION NUMBER: 09/377,310
PRIOR FILING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 37
LENGTH: 15
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: antisense sequence
PCT-US00-18999-37

Query Match 75.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.2e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 tctcgtcgtcgtg 17
||||| ||| |||
DB 1 tctcgtcgtcgtg 15

RESULT 6

US-09-377-310-37
Sequence 37, Application US/09377310A
GENERAL INFORMATION:
APPLICANT: Monia, Brett P.
APPLICANT: Gaarde, William A.
TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
FILE REFERENCE: ISPH-0389
CURRENT APPLICATION NUMBER: US/09/377,310A
CURRENT FILING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 37
LENGTH: 15
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: antisense sequence
US-09-377-310-37

Query Match 75.0%; Score 15; DB 17; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.2e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 tctcgtcgtcgtg 17
||||| ||| |||
DB 1 tctcgtcgtcgtg 15

RESULT 7

US-09-757-100B-37
Sequence 37, Application US/09757100B
GENERAL INFORMATION:
APPLICANT: Monia, Brett P.
APPLICANT: Gaarde, William A.
APPLICANT: Nero, Pamela S.
TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
FILE REFERENCE: ISPH-0533
CURRENT APPLICATION NUMBER: US/09/757,100B
CURRENT FILING DATE: 2001-03-15
PRIOR APPLICATION NUMBER: 09/377,310
PRIOR FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/US00/18999
PRIOR FILING DATE: 2000-07-13
NUMBER OF SEQ ID NOS: 44
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 37
LENGTH: 15
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: antisense sequence
US-09-757-100B-37

Query Match 75.0%; Score 15; DB 29; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.2e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 tctcgtcgtcgtg 17
||||| ||| |||
DB 1 tctcgtcgtcgtg 15

RESULT 8

US-09-144-428-31
Sequence 31, Application US/09144428
GENERAL INFORMATION:
APPLICANT: BAYER CORPORATION, The
APPLICANT: TAMBURINI, Paul P
APPLICANT: DAVIS, Gary
APPLICANT: DELARIA, Katherine A
APPLICANT: MARLOR, Christopher W
APPLICANT: MULLER, Daniel K
TITLE OF INVENTION: HUMAN BIKUNIN
NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 S. Wacker Drive Suite 3200
CITY: CHICAGO
STATE: ILLINOIS
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/144,428
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/03894
FILING DATE: 10-MAR-1997

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/013,106
FILING DATE: 11-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/019,793
FILING DATE: 14-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/725,251
FILING DATE: 04-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: CHAO, Mark
REGISTRATION NUMBER: 37,293
REFERENCE/DOCKET NUMBER: 96,223-II
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 913-0001
TELEFAX: (312) 913-0002
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
US-09-144-428-31

Query Match 74.0%; Score 14.8; DB 15; Length 35;
Best Local Similarity 88.9%; Pred. No. 9.3e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 tctctgctgctggtgaa 20
||||| ||||||| |||||
Db 6 TCCTCACTGCTGCGGAA 23

RESULT 9

US-09-218-913B-31
Sequence 31, Application US/09218913B
GENERAL INFORMATION:
APPLICANT: Hall, Roderick L.
APPLICANT: Poll, Christopher T.
APPLICANT: Newton, Benjamin B.
APPLICANT: Taylor, William J.A.
TITLE OF INVENTION: A Method for Accelerating the Rate of Mucociliary Clearance
FILE REFERENCE: 98,736
CURRENT APPLICATION NUMBER: US/09/218,913B
CURRENT FILING DATE: 1998-12-22
NUMBER OF SEQ ID NOS: 71
SOFTWARE: Microsoft Word 97
SEQ ID NO 31
LENGTH: 35
TYPE: DNA
ORGANISM: S. cerevisiae
US-09-218-913B-31

Query Match 74.0%; Score 14.8; DB 16; Length 35;
Best Local Similarity 88.9%; Pred. No. 9.3e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 tctctgctgctggtgaa 20
||||| ||||||| |||||
Db 6 tctctactgctgctgaa 23

RESULT 10

US-09-441-966-31
Sequence 31, Application US/09441966
GENERAL INFORMATION:
APPLICANT: Hall, Roderick L.
APPLICANT: Poll, Christopher T.
APPLICANT: Newton, Benjamin B.

APPLICANT: Taylor, William J.A.
TITLE OF INVENTION: A Method for Accelerating the Rate of Mucociliary Clearance
FILE REFERENCE: 98,736-A
CURRENT APPLICATION NUMBER: US/09/441,966
CURRENT FILING DATE: 1999-11-17
PRIOR APPLICATION NUMBER: 09/218,913
PRIOR FILING DATE: 1998-12-22
NUMBER OF SEQ ID NOS: 71
SOFTWARE: Microsoft Word 97
SEQ ID NO 31
LENGTH: 35
TYPE: DNA
ORGANISM: S. cerevisiae
US-09-441-966-31

Query Match 74.0%; Score 14.8; DB 18; Length 35;
Best Local Similarity 88.9%; Pred. No. 9.3e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 tctctgctgctggtgaa 20
||||| ||||||| |||||
Db 6 tctctactgctgctgaa 23

RESULT 11

US-08-472-801-1314
Sequence 1314, Application US/08472801
GENERAL INFORMATION:
APPLICANT: Hessed 2
APPLICANT: Smith, Larry J.
TITLE OF INVENTION: Method and Compositions for Cellular Reprogramming
FILE REFERENCE: Hessed 2
CURRENT APPLICATION NUMBER: US/08/472,801
CURRENT FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 3601
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1314
LENGTH: 37
TYPE: DNA
ORGANISM: Homo sapiens
US-08-472-801-1314

Query Match 72.0%; Score 14.4; DB 8; Length 37;
Best Local Similarity 93.8%; Pred. No. 1.4e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 tctctgctgctggtgg 18
||||| ||||||| |||||
Db 5 tctctgctgctgctgg 20

RESULT 12

US-08-668-235-1314
Sequence 1314, Application US/08668235
GENERAL INFORMATION:
APPLICANT: Larry J. Smith
TITLE OF INVENTION: Methods and Compositions for Cellular Reprogramming
FILE REFERENCE: Hessed-1
CURRENT APPLICATION NUMBER: US/08/668,235
CURRENT FILING DATE: 1996-06-17
EARLIER APPLICATION NUMBER: 07/748,997
EARLIER FILING DATE: 08/23/91
EARLIER APPLICATION NUMBER: 08/426,781
EARLIER FILING DATE: 04/22/95
EARLIER APPLICATION NUMBER: 08/472,801
EARLIER FILING DATE: 06/07/95
NUMBER OF SEQ ID NOS: 3629
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1314

```

; LENGTH: 37
; TYPE: DNA
; ORGANISM: Homo sapiens
US-08-668-235-1314

```

Query Match 72.0%; Score 14.4; DB 10; Length 37;
Best Local Similarity 93.8%; Pred. NO. 1.4e+04;
Matches 15; Conservative 0; Mismatches 1; Indels

Qy 3 tctcgcgtgctggtgg 18
 | | | | | | | | |
Dd 5 tctcgcgtgctgctgg 20

```

RESULT 13
PCT-US97-06104-16/c
; Sequence 16, Application PC/TUS9706104
; GENERAL INFORMATION:
; APPLICANT: University of Massachusetts
; TITLE OF INVENTION: OLIGONUCLEOTIDES WITH ANTI-EPSTEIN-BARR
; TITLE OF INVENTION: VIRUS ACTIVITY
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804

```

Query Match 71.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.7e+04;
Matches 16; Conservative 0; Mismatches 3; Indels

Qy 2 ttctctgctgctggtgga 20
|| ||||| ||||| |||||
Db 20 TTGCTCGCAGCTGGAGGA 2

RESULT 14
US-60-232-638-132115
; Sequence 132115, Application US/60232638
; GENERAL INFORMATION;

```

; APPLICANT: Mittmann
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of Yeast
; FILE REFERENCE: 3110
; CURRENT APPLICATION NUMBER: US/60/232,638
; CURRENT FILING DATE: 2000-09-14
; NUMBER OF SEQ ID NOS: 138410
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 132115
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces Cerevisiae
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: SGD YPL144W
US-60-232-638-132115

```

Query Match	68.0%	Score 13.6;	DB 55;	Length 25;
Best Local Similarity	80.0%;	Pred. No. 3.3e+4;		
Matches 16;	Conservative	0;	Mismatches 4;	Gaps 0;
			Indels	0;

Qy 1 attcctcgctgctggtgaa 20
||| ||||| ||||| ||
Db 6 atccqctcactactggtgaa 25

```

RESULT 15
US-60-234-017-326383/c
; Sequence 326383, Application US/60234017
; GENERAL INFORMATION:
; APPLICANT: Mittmann, M
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of Mus
; TITLE OF INVENTION: musculus
; FILE REFERENCE: 3115
; CURRENT APPLICATION NUMBER: US/60/234,017
; CURRENT FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 605887
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 326383
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank AA153229
US-60-234-017-326383

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Query Match 68.0%; Score 13.6; DB 55; Length 25;
Best Local Similarity 80.0%; Pred. No. 3.3e+04;
Matches 16: Conservative 0; Mismatches 4; Indels

QY 1 attcctcgtcgtggtgga 20
||||| ||||| ||||| ||||| |||||
Db 22 ATTCCACGCTACTCGTGCAA 3

Search completed: October 2, 2001, 21:50:18
Job time: 24531 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 2, 2001, 16:55:05 ; Search time 2173.58 Seconds
(without alignments)
19.290 Million cell updates/sec

Title: US-09-757-100B-17

Perfect score: 20

Sequence: 1 attctcgtctgctggaa 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1895189 seqs, 1048201267 residues

Total number of hits satisfying chosen parameters: 299022

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_NA_New.*
1: /cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq.*
2: /cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq.*
3: /cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq.*
4: /cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq.*
5: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq.*
6: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq.*
7: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq.*
8: /cgn2_6/ptodata/2/pna/US60_NEW_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	14	70.0	18	6	US-09-477-962-58
C 2	13.4	67.0	20	6	US-09-766-450-39
C 3	13.4	67.0	20	6	US-09-198-452A-5835
C 4	13.4	67.0	44	8	US-60-253-456-27973
C 5	13	65.0	31	6	US-09-801-274-757
C 6	12.8	64.0	17	5	US-09-371-772B-6946
C 7	12.8	64.0	17	5	US-09-708-690-6946
C 8	12.8	64.0	17	5	US-09-708-690-9123
C 9	12.8	64.0	47	6	US-60-252-833-5936
C 10	12.6	63.0	20	6	US-09-198-452A-6492
C 11	12.6	63.0	24	7	US-09-912-935-48
C 12	12.4	62.0	31	6	US-09-801-274-638
C 13	12.4	62.0	38	6	US-09-546-745A-4473
C 14	12.4	62.0	38	8	US-60-278-232-3939
C 15	12.4	62.0	48	7	US-09-864-785-3115
C 16	12.2	61.0	31	5	US-09-574-376B-160
C 17	12	60.0	16	5	US-09-371-772B-5835
C 18	12	60.0	16	5	US-09-708-690-5835
C 19	12	60.0	17	5	US-09-371-772B-4795
C 20	12	60.0	17	5	US-09-371-772B-4796
C 21	12	60.0	17	5	US-09-371-772B-4797
C 22	12	60.0	17	5	US-09-371-772B-6943
C 23	12	60.0	17	5	US-09-371-772B-6944
C 24	12	60.0	17	5	US-09-371-772B-6945
C 25	12	60.0	17	5	US-09-708-690-4795

C 26	12	60.0	17	5	US-09-708-690-4796	Sequence 4796, Ap
C 27	12	60.0	17	5	US-09-708-690-4797	Sequence 4797, Ap
C 28	12	60.0	17	5	US-09-708-690-6943	Sequence 6943, Ap
C 29	12	60.0	17	5	US-09-708-690-6944	Sequence 6944, Ap
C 30	12	60.0	17	5	US-09-708-690-6945	Sequence 6945, Ap
C 31	12	60.0	17	5	US-09-708-690-7664	Sequence 7664, Ap
C 32	12	60.0	17	5	US-09-708-690-7665	Sequence 7665, Ap
C 33	11.8	59.0	18	7	US-09-787-252-44	Sequence 44, Appl
C 34	11.8	59.0	20	6	US-09-198-452A-6820	Sequence 6820, Ap
C 35	11.8	59.0	48	5	US-09-532-537B-2863	Sequence 2863, Ap
C 36	11.8	59.0	48	7	US-09-864-785-3510	Sequence 3510, Ap
C 37	11.6	58.0	20	6	US-09-198-452A-4453	Sequence 4453, Ap
C 38	11.6	58.0	38	6	US-09-535-373-54	Sequence 54, Appl
C 39	11.6	58.0	48	6	US-09-509-098-71	Sequence 71, Appl
C 40	11.4	57.0	21	6	US-09-508-891-16	Sequence 16, Appl
C 41	11.4	57.0	22	5	US-09-931-700-11	Sequence 11, Appl
C 42	11.4	57.0	25	5	US-09-828-313-84	Sequence 84, Appl
C 43	11.4	57.0	27	5	US-09-622-646-9	Sequence 9, Appl
C 44	11.4	57.0	31	6	US-09-801-274-122	Sequence 122, App
C 45	11.4	57.0	31	6	US-09-801-274-1390	Sequence 1390, Ap

ALIGNMENTS

RESULT 1
US-09-477-962-58/c
; Sequence 58, Application US/09477962
; GENERAL INFORMATION:
; APPLICANT: SHEN, BEN
; APPLICANT: DU, LIANGCHENG
; APPLICANT: SANCHEZ, CESAR
; APPLICANT: CHEN, MEI
; APPLICANT: EDWARDS, DANIEL J.
; TITLE OF INVENTION: BLEOMYCIN GENE CLUSTER COMPONENTS AND THEIR USES
; FILE REFERENCE: 407T-895820US
; CURRENT APPLICATION NUMBER: US/09/477,962
; CURRENT FILING DATE: 2000-01-05
; PRIOR APPLICATION NUMBER: 60/115,435
; PRIOR FILING DATE: 1999-01-06
; PRIOR APPLICATION NUMBER: 60/118,848
; PRIOR FILING DATE: 1999-02-05
; NUMBER OF SEQ ID NOS: 133
; SOFTWARE: PatentIn Ver. 3.0
; SEQ ID NO 58
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-477-962-58

Query Match 70.0%; Score 14; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 cctcgtctgctgggtg 17
|||||
Db 17 CCTCGTCTGCTGGTG 4

RESULT 2
US-09-766-450-39/c
; Sequence 39, Application US/09766450
; GENERAL INFORMATION:
; APPLICANT: Collins, Colin
; APPLICANT: Vollik, Stanislav
; APPLICANT: Gray, Joe W.
; APPLICANT: Albertson, Donna G.
; APPLICANT: Pinkel, Daniel
; TITLE OF INVENTION: Repeat-Free Probes for Molecular

; TITLE OF INVENTION: Cytogenetics
; FILE REFERENCE: 023071-111800US
; CURRENT APPLICATION NUMBER: US/09/766,450
; CURRENT FILING DATE: 2001-01-19
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 39
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer 727725.fl
US-09-766-450-39

Query Match 67.0%; Score 13.4; DB 6; Length 20;
Best Local Similarity 93.3%; Pred. No. 3.6e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 attctcgtcgtcgtg 15
||||| |||||||
Db 19 ATTCTCCTCGTCTGG 5

RESULT 3
US-09-198-452A-5835/c
; Sequence 5835, Application US/09198452A
; GENERAL INFORMATION:
; APPLICANT: Griffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 5835
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-5835

Query Match 67.0%; Score 13.4; DB 6; Length 20;
Best Local Similarity 93.3%; Pred. No. 3.6e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 attctcgtcgtcgtg 15
||||| |||||||
Db 19 ACTCCTCGTCTGG 5

RESULT 4
US-60-253-456-27973
; Sequence 27973, Application US/60253456
; GENERAL INFORMATION:
; APPLICANT: Havukkala, Ilkka J
; TITLE OF INVENTION: Polynucleotides, isolated from
; TITLE OF INVENTION: plants, and methods for their use.
; FILE REFERENCE: 1054PI
; CURRENT APPLICATION NUMBER: US/60/253,456
; CURRENT FILING DATE: 2000-11-27
; NUMBER OF SEQ ID NOS: 37096
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27973
; LENGTH: 44
; TYPE: DNA
; ORGANISM: Pinus radiata
US-60-253-456-27973

Query Match 67.0%; Score 13.4; DB 8; Length 44;
Best Local Similarity 93.3%; Pred. No. 4e+03;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 3 tctcgtcgtcgtg 17
||||| |||||||
Db 22 tctcgtcgtcgtg 36

RESULT 5
US-09-801-274-757/c
; Sequence 757, Application US/09801274
; GENERAL INFORMATION:
; APPLICANT: Cargill, Michele
; APPLICANT: Ireland, James S.
; APPLICANT: Lander, Eric S.
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: 2825-2009-001
; CURRENT APPLICATION NUMBER: US/09/801,274
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: US 60/187,510
; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: US 60/206,129
; PRIOR FILING DATE: 2000-05-22
; NUMBER OF SEQ ID NOS: 1802
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 757
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-801-274-757

Query Match 65.0%; Score 13; DB 6; Length 31;
Best Local Similarity 86.7%; Pred. No. 6e+03;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 tctcgtcgtcgtg 17
:||||| |||||
Db 16 KCCTCGTCTGCTG 2

RESULT 6
US-09-371-772B-6946/c
; Sequence 6946, Application US/09371772B
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions
; FILE REFERENCE: MBHB00, 876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6946
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-6946

Query Match 64.0%; Score 12.8; DB 5; Length 17;
Best Local Similarity 87.5%; Pred. No. 7e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 ctcgctcgtcgtgaa 20
|| |||||||

Db 17 CTTCTGCTGCTGGAA 2

RESULT 7
US-09-708-690-6946/c
; Sequence 6946, Application US/09708690
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MHB00,876-L (400/002)
; CURRENT APPLICATION NUMBER: US/09/708,690
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; PRIOR APPLICATION NUMBER: US 09/371,772
; PRIOR FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 09/685,664
; PRIOR FILING DATE: 2000-10-10
; NUMBER OF SEQ ID NOS: 20828
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6946
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-708-690-6946

Query Match 64.0%; Score 12.8; DB 5; Length 17;
Best Local Similarity 87.5%; Pred. No. 7e+03; Length 17;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 ctgcgtcgtcgtgga 20
||| ||||| |||||
Db 17 CTTCTGCTGCTGGAA 2

RESULT 8
US-09-708-690-9123/c
; Sequence 9123, Application US/09708690
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MHB00,876-L (400/002)
; CURRENT APPLICATION NUMBER: US/09/708,690
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; PRIOR APPLICATION NUMBER: US 09/371,772
; PRIOR FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 09/685,664
; PRIOR FILING DATE: 2000-10-10
; NUMBER OF SEQ ID NOS: 20828
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9123
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid

US-09-708-690-9123

Query Match 64.0%; Score 12.8; DB 5; Length 17;
Best Local Similarity 87.5%; Pred. No. 7e+03; Length 17;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 ctgcgtcgtcgtgga 20
||| ||||| |||||
Db 16 CTTCTGCTGCTGGAA 1

RESULT 9
US-60-252-833-5936/c
; Sequence 5936, Application US/60252833
; GENERAL INFORMATION:
; APPLICANT: Glenn, Matthew
; APPLICANT: Grigor, Murray R
; TITLE OF INVENTION: Compositions isolated from bovine
; TITLE OF INVENTION: tissues and methods for their use.
; FILE REFERENCE: 1052P2
; CURRENT APPLICATION NUMBER: US/60/252,833
; CURRENT FILING DATE: 2000-11-21
; NUMBER OF SEQ ID NOS: 43535
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5936
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Bovine
US-60-252-833-5936

Query Match 64.0%; Score 12.8; DB 8; Length 47;
Best Local Similarity 87.5%; Pred. No. 7.8e+03; Length 47;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ttctcgtcgtcgtggtg 17
||| ||||| |||||
Db 27 TTCATCGCTGCTGCTG 12

RESULT 10
US-09-198-452A-6492
; Sequence 6492, Application US/09198452A
; GENERAL INFORMATION:
; APPLICANT: Griffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragme
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, pr
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 6492
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-6492

Query Match 63.0%; Score 12.6; DB 6; Length 20;
Best Local Similarity 78.9%; Pred. No. 8.9e+03; Length 20;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 attctcgtcgtcgtgga 19
| ||||| ||||| |||
Db 2 agtctcgtcgtgataga 20

RESULT 11
US-09-912-935-48/c
; Sequence 48, Application US/09912935
; GENERAL INFORMATION:

; APPLICANT: Nishikawa, Mitsuo et al.
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE
; FILE REFERENCE: 32066/37483
; CURRENT APPLICATION NUMBER: US/09/912,935
; CURRENT FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: PCT/US00/35260
; PRIOR FILING DATE: 2000-12-23
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 48
; LENGTH: 24
; TYPE: DNA
; ORGANISM: primer H2728F
US-09-912-935-48

Query Match 63.0%; Score 12.6; DB 7; Length 24;
Best Local Similarity 78.9%; Pred. No. 9.1e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 ttctcgtcgtcgttgaa 20
||| ||||| ||| |||||
Db 21 TTTCTCGCAGCCGAGGAA 3

RESULT 12
US-09-801-274-638
; Sequence 638, Application US/09801274
; GENERAL INFORMATION:
; APPLICANT: Cargill, Michele
; APPLICANT: Ireland, James S.
; APPLICANT: Lander, Eric S.
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: 2825 2009-001
; CURRENT APPLICATION NUMBER: US/09/801,274
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: US 60/187,510
; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: US 60/206,129
; PRIOR FILING DATE: 2000-05-22
; NUMBER OF SEQ ID NOS: 1802
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 638
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-801-274-638

Query Match 62.0%; Score 12.4; DB 6; Length 31;
Best Local Similarity 81.2%; Pred. No. 1.2e+04;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 5 ctccgtcgtcgttgaa 20
||| ||||| ||| |||||
Db 5 ctccctcgtcgttgaa 20

RESULT 13
US-09-546-745A-4473
; Sequence 4473, Application US/09546745A
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: Zwick, Michael
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Regulation of Repressor Genes using Nucleic Acid Molecules
; FILE REFERENCE: 237/193
; CURRENT APPLICATION NUMBER: US/09/546,745A
; CURRENT FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 7043

; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4473
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
; NAME/KEY: misc_feature
; LOCATION: (17)..(26)
; OTHER INFORMATION: positions 17-26 n stands for any nucleotide, positions 19-26 n
; OTHER INFORMATION: be optionally absent
US-09-546-745A-4473

Query Match 62.0%; Score 12.4; DB 6; Length 38;
Best Local Similarity 64.3%; Pred. No. 1.2e+04;
Matches 9; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 4 cctcgtcgtcgtg 17
||| ||||| ||| |||||
Db 1 ccucgucgucgaug 14

RESULT 14
US-60-278-232-3939
; Sequence 3939, Application US/60278232
; GENERAL INFORMATION:
; APPLICANT: Morris, MacDonald
; APPLICANT: Lal, Preeti
; APPLICANT: Diep, Dinh
; TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
; TITLE OF INVENTION: Polynucleotide Sequence Databases, and Single Nucleotide
; FILE REFERENCE: GX-0011 P
; CURRENT APPLICATION NUMBER: US/60/278,232
; CURRENT FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 12,557
; SOFTWARE: PERL Program
; SEQ ID NO 3939
; LENGTH: 38
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: SNP00049413
; NAME/KEY: snp
; LOCATION: 26
; OTHER INFORMATION: 229881.1, 569, T->C
US-60-278-232-3939

Query Match 62.0%; Score 12.4; DB 8; Length 38;
Best Local Similarity 92.9%; Pred. No. 1.2e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 attcctcgtcgtg 14
||| ||||| |||||
Db 23 attcctcgtcgtg 36

RESULT 15
US-09-864-785-3115
; Sequence 3115, Application US/09864785
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Draper, Ken
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Rel
; TITLE OF INVENTION: Levels of NF-Kappa B
; FILE REFERENCE: 400/022 (MBH00-812-D)
; CURRENT APPLICATION NUMBER: US/09/864,785
; CURRENT FILING DATE: 2001-05-23

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; NUMBER OF SEQ ID NOS: 3929
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3115
; LENGTH: 48
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-864-785-3115

Query Match      62.0%; Score 12.4; DB 7; Length 48;
Best Local Similarity 78.6%; Pred. No. 1.2e+04;
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 7 cgctgctggtgga 20
Db 2 cgugcugaggaa 15

Search completed: October 2, 2001, 16:55:05
Job time: 17668 sec
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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: October 2, 2001, 16:55:04 ; Search time 2173.58 Seconds
(without alignments)
19.290 Million cell updates/sec

Title: US-09-757-100B-16

Perfect score: 20

Sequence: 1 ctaggggaggctcagtgtgg 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1895189 seqs, 1048201267 residues

Total number of hits satisfying chosen parameters: 299022

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c 2	12.6	63.0	26	7	US-09-922-146-6
c 3	12.6	63.0	32	6	US-09-545-777-8
c 4	12.2	61.0	31	6	US-09-817-879-5909
c 5	12	60.0	37	5	US-09-708-690-18238
c 6	12	60.0	38	5	US-09-942-325-6
c 7	11.8	59.0	22	6	US-09-883-152-59
c 8	11.8	59.0	31	5	US-09-574-376B-1160
c 9	11.8	59.0	31	5	US-09-574-376B-1320
c 10	11.8	59.0	39	5	US-09-771-372-9
c 11	11.6	58.0	31	1	PCT-US01-19353-77
c 12	11.6	58.0	31	7	US-09-786-033-19
c 13	11.6	58.0	39	7	US-09-514-673-26
c 14	11.6	58.0	40	7	US-09-563-794-69
c 15	11.4	57.0	30	5	US-09-310-735A-140
c 16	11.4	57.0	30	5	US-09-310-735A-151
c 17	11.4	57.0	30	5	US-09-310-844B-140
c 18	11.4	57.0	30	5	US-09-310-844B-151
c 19	11.2	56.0	17	7	US-09-818-875-1934
c 20	11.2	56.0	17	7	US-09-818-875-1935
c 21	11.2	56.0	20	6	US-09-421-971-19
c 22	11.2	56.0	20	6	US-09-527-376-6
c 23	11.2	56.0	20	7	US-09-906-158-111
c 24	11.2	56.0	21	6	US-09-765-081-81
c 25	11.2	56.0	22	5	US-09-941-992-470

ALIGNMENTS

RESULT 1

US-09-650-012A-1062/c
; Sequence 1062, Application US/09650012A
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Jarvis, Thale
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Induction of Graft Tolerance and Re
; TITLE OF INVENTION: Immune Responses
; FILE REFERENCE: 250/130 (MBHB00-900-A)
; CURRENT APPLICATION NUMBER: US/09/650,012A
; CURRENT FILING DATE: 2000-08-28
; PRIOR APPLICATION NUMBER: US 08/585,684
; PRIOR FILING DATE: 1996-01-12
; PRIOR APPLICATION NUMBER: US 60/000,951
; PRIOR FILING DATE: 1995-07-07
; PRIOR APPLICATION NUMBER: US 09/038,073
; PRIOR FILING DATE: 1998-03-11
; NUMBER OF SEQ ID NOS: 2285
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1062
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-650-012A-1062

Query Match 66.0%; Score 13.2; DB 5; Length 18;
Best Local Similarity 83.3%; Pred. No. 5.7e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ctaggggaggctcagtgt 18

Db 18 CTGGGGGAGGCTGAGGGT 1

RESULT 2

US-09-922-146-6/c
; Sequence 6, Application US/09922146
; GENERAL INFORMATION:
; APPLICANT: Lex M. Cowsett
; APPLICANT: Brett P. Monia
; TITLE OF INVENTION: ANTISENSE MODULATION OF DUAL SPECIFIC PHOSPHATASE 9 EXPRESSION
; FILE REFERENCE: RPS-0252
; CURRENT APPLICATION NUMBER: US/09/922,146
; CURRENT FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 48

; SEQ ID NO 6
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR Probe
US-09-922-146-6

Query Match 63.0%; Score 12.6; DB 7; Length 26;
Best Local Similarity 78.9%; Pred. No. 1.1e+04;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 2 tagggaggctcagtggtg 20
| | | | | | | | | | | | | | | | | | | | | |
Db 19 TAGCGGATCCCGAGTTGG 1

RESULT 3
US-09-545-777-8/c
; Sequence 8, Application US/09545777
; GENERAL INFORMATION:
; APPLICANT: Xu, Hua
; APPLICANT: Jarnigan, Kurt
; APPLICANT: Zhou, Hua
; APPLICANT: Greene L., Amy
; APPLICANT: Thode, Silke
; TITLE OF INVENTION: METHODS AND NUCLEIC ACID VECTORS FOR RAPID AND PARALLEL
; TITLE OF INVENTION: ASSAY DEVELOPMENT, FOR CHARACTERIZATION OF THE
; TITLE OF INVENTION: ACTIVITIES OF BIOLOGICAL RESPONSE MODIFIERS
; FILE REFERENCE: 5050-0015
; CURRENT APPLICATION NUMBER: US/09/545,777
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 60/128,631
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 8
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer TK3
US-09-545-777-8

Query Match 63.0%; Score 12.6; DB 6; Length 32;
Best Local Similarity 78.9%; Pred. No. 1.1e+04;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 2 tagggaggctcagtggtg 20
| | | | | | | | | | | | | | | | | | | | | |
Db 26 TGGGGGAGGCTAACTAGG 8

RESULT 4
US-09-817-879-5909/c
; Sequence 5909, Application US/09817879
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
; TITLE OF INVENTION: Hepatitis C Virus Infection
; FILE REFERENCE: MBHB00-801-F
; CURRENT APPLICATION NUMBER: US/09/817,879
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9703
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5909
; LENGTH: 31
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature

; LOCATION:
; OTHER INFORMATION: DNazyme
US-09-817-879-5909

Query Match 61.0%; Score 12.2; DB 6; Length 31;
Best Local Similarity 82.4%; Pred. No. 1.7e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 4 ggggaggctcagtggtg 20
| | | | | | | | | | | | | | | | | | | | | |
Db 31 GGGGAGGCTCGTGTGTAG 15

RESULT 5
US-09-708-690-18238
; Sequence 18238, Application US/09708690
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwigen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00,876-L (400/002)
; CURRENT APPLICATION NUMBER: US/09/708,690
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; PRIOR APPLICATION NUMBER: US 09/371,772
; PRIOR FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 09/685,664
; PRIOR FILING DATE: 2000-10-10
; NUMBER OF SEQ ID NOS: 20828
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 18238
; LENGTH: 37
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-708-690-18238

Query Match 60.0%; Score 12; DB 5; Length 37;
Best Local Similarity 60.0%; Pred. No. 2.2e+04;
Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Oy 1 ctaggggaggctcagtggtg 20
| | | | | | | | | | | | | | | | | | | | | |
Db 18 cgagugaggucucagugug 37

RESULT 6
US-09-942-325-6/c
; Sequence 6, Application US/09942325
; GENERAL INFORMATION:
; APPLICANT: Iacovitti, Lorraine
; APPLICANT: Kessler, Mark
; TITLE OF INVENTION: The Human Tyrosine Hydroxylase Promoter
; TITLE OF INVENTION: Sequence and Related Methods and Compositions
; FILE REFERENCE: IAC01.NP001
; CURRENT APPLICATION NUMBER: US/09/942,325
; CURRENT FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: 60/228931
; PRIOR FILING DATE: 2000-02-30
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 38

; TYPE: DNA
; ORGANISM: Homo sapien
US-09-942-325-6

Query Match 60.0%; Score 12; DB 5; Length 38;
Best Local Similarity 100.0%; Pred. No. 2.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 ggcctcagtggtg 20
|||||
Db 34 GGCTCAGTGTGG 23

RESULT 7

US-09-883-152-59
; Sequence 59, Application US/09883152
; GENERAL INFORMATION:
; APPLICANT: Kennedy, Giulia
; APPLICANT: Kang, Sanmao
; APPLICANT: Reinhard, Christoph
; APPLICANT: Jefferson, Anne Bennett
; TITLE OF INVENTION: POLYNUCLEOTIDES RELATED TO COLON CANCER
; FILE REFERENCE: 2300-1663
; CURRENT APPLICATION NUMBER: US/09/883,152
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/211,835
; PRIOR FILING DATE: 2000-06-15
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 59
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-883-152-59

Query Match 59.0%; Score 11.8; DB 6; Length 22;
Best Local Similarity 86.7%; Pred. No. 2.7e+04;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 aggggaggtcagtg 17
|||||
Db 8 aggggaggtcagtg 22

RESULT 8

US-09-574-376B-1160
; Sequence 1160, Application US/09574376B
; GENERAL INFORMATION:
; APPLICANT: Warrington, Janet
; APPLICANT: Shah, Nila
; APPLICANT: Gingeras, Thomas Raymond
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Human Lymphoblast Polymorphisms
; FILE REFERENCE: 3229.2
; CURRENT APPLICATION NUMBER: US/09/574,376B
; CURRENT FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 1330
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1160
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
US-09-574-376B-1160

Query Match 59.0%; Score 11.8; DB 5; Length 31;
Best Local Similarity 76.5%; Pred. No. 2.7e+04;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 ctaggggaggtcagtg 17
|||||
Db 14 ctmggggtcggtcagtg 30

RESULT 9

US-09-574-376B-1320
; Sequence 1320, Application US/09574376B
; GENERAL INFORMATION:
; APPLICANT: Warrington, Janet
; APPLICANT: Shah, Nila
; APPLICANT: Gingeras, Thomas Raymond
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Human Lymphoblast Polymorphisms
; FILE REFERENCE: 3229.2
; CURRENT APPLICATION NUMBER: US/09/574,376B
; CURRENT FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 1330
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1320
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
US-09-574-376B-1320

Query Match 59.0%; Score 11.8; DB 5; Length 31;
Best Local Similarity 76.5%; Pred. No. 2.7e+04;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 ggggaggtcagtg 20
|||||
Db 6 ggtcggtcggtcagtg 22

RESULT 10

US-09-771-372-9
; Sequence 9, Application US/09771372
; GENERAL INFORMATION:
; APPLICANT: LOEHRLEIN, CHRISTINE
; APPLICANT: POLLART, DAN
; APPLICANT: SHALER, THOMAS
; APPLICANT: STEPHENS, KATHY
; APPLICANT: TAN, YUPING
; APPLICANT: WONG, LINDA
; APPLICANT: MONFORTE, JOSEPH
; TITLE OF INVENTION: METHODS FOR ANALYSIS OF GENE EXPRESSION
; FILE REFERENCE: 14-004510US
; CURRENT APPLICATION NUMBER: US/09/771,372
; CURRENT FILING DATE: 2001-01-27
; PRIOR APPLICATION NUMBER: 60/119,006
; PRIOR FILING DATE: 2000-01-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 39
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-771-372-9

Query Match 59.0%; Score 11.8; DB 5; Length 39;
Best Local Similarity 86.7%; Pred. No. 2.7e+04;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 gggaggtcagtg 19
|||||
Db 16 gggaggtcagtg 30

```
RESULT 11
PCT-US01-19353-77
; Sequence 77, Application PC/TUS0119353
; GENERAL INFORMATION:
; APPLICANT: Anthony, James
; APPLICANT: Lorincz, Attila
; APPLICANT: Williams, Inna
; APPLICANT: Troy, John
; APPLICANT: Tang, Yanlin
; TITLE OF INVENTION: DETECTION OF NUCLEIC ACIDS BY TYPE-SPECIFIC HYBRID
; FILE REFERENCE: 2629-4017PCT
; CURRENT APPLICATION NUMBER: PCT/US01/19353
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 09/594,839
; PRIOR FILING DATE: 2000-06-15
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 77
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: DP-1
; OTHER INFORMATION: Description of Artificial Sequence:nucleic acid
; OTHER INFORMATION: probe
PCT-US01-19353-77

Query Match 58.0%; Score 11.6; DB 1; Length 31;
Best Local Similarity 77.8%; Pred. No. 3.4e+04;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 tagggaggctcagtg 19
||| ||||| |||
Db 5 taggtgaggctcagtg 22

RESULT 12
US-09-786-033-19
; Sequence 19, Application US/09786033
; GENERAL INFORMATION:
; APPLICANT: Pausch, Mark Henry
; APPLICANT: Weiss, Jurgen
; TITLE OF INVENTION: METHODS FOR IMPROVING THE FUNCTION OF HETEROLOGOUS G
; FILE REFERENCE: 01142.102-00304
; CURRENT APPLICATION NUMBER: US/09/786,033
; CURRENT FILING DATE: 2001-07-03
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: oligonucleotide
US-09-786-033-19

Query Match 58.0%; Score 11.6; DB 7; Length 31;
Best Local Similarity 77.8%; Pred. No. 3.4e+04;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 tagggaggctcagtg 19
||| ||||| |||
Db 12 tacagatggctcagtg 29

RESULT 13
US-09-514-673-26/c
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; Sequence 26, Application US/09514673
; GENERAL INFORMATION:
; APPLICANT: DOWDY, STEVEN F.
; TITLE OF INVENTION: NOVEL TRANSDUCTION MOLECULES AND METHODS FOR USING SAME
; FILE REFERENCE: 49054(71742)
; CURRENT APPLICATION NUMBER: US/09/514,673
; CURRENT FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: 60/122,757
; PRIOR FILING DATE: 1999-02-28
; PRIOR APPLICATION NUMBER: 60/151,291
; PRIOR FILING DATE: 1999-08-29
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 39
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-514-673-26
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Query Match 58.0%; Score 11.6; DB 7; Length 39;
Best Local Similarity 77.8%; Pred. No. 3.4e+04;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 tagggaggctcagtg 19
||| ||||| |||
Db 33 TGGGGGAGGCTAACTGAG 16
```

```
RESULT 14
US-09-563-794-69/c
; Sequence 69, Application US/09563794
; GENERAL INFORMATION:
; APPLICANT: Kruger, Martin
; APPLICANT: Welch, Peter J.
; APPLICANT: Barber, Jack R.
; TITLE OF INVENTION: Cellular Regulators of Infectious Agents and Methods of
; TITLE OF INVENTION: Use
; FILE REFERENCE: P-IU 3738
; CURRENT APPLICATION NUMBER: US/09/563,794
; CURRENT FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 69
; LENGTH: 40
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-563-794-69
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Query Match 58.0%; Score 11.6; DB 7; Length 40;
Best Local Similarity 77.8%; Pred. No. 3.4e+04;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 tagggaggctcagtg 19
||| ||||| |||
Db 33 TGGGGGAGGCTAACTGAG 16
```

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RESULT 15
US-09-310-735A-140/G
; Sequence 140, Application US/09310735A
; GENERAL INFORMATION:
; APPLICANT: Ecker, David J
; APPLICANT: Griffey, Richard
; APPLICANT: Crooke, Stanley T
; APPLICANT: Sampath, Ranga
; APPLICANT: Swayze, Eric
```

; APPLICANT: Mohan, Venkatraman
; APPLICANT: Hofstadler, Steven
; APPLICANT: McNeil, John
; TITLE OF INVENTION: Modulation of Molecular Interaction Sites on RNA and
; FILE REFERENCE: Other Biomolecules
; CURRENT APPLICATION NUMBER: US/09/310,735A
; CURRENT FILING DATE: 1999-05-12
; PRIOR APPLICATION NUMBER: 09/076,404
; PRIOR FILING DATE: 1998-05-12
; NUMBER OF SEQ ID NOS: 393
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 140
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Novel Sequence
US-09-310-735A-140

Query Match 57.0%; Score 11.4; DB 5; Length 30;
Best Local Similarity 92.3%; Pred. No. 4.2e+04;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 8 aggtcagtggtg 20
|| |||||
Db 14 AGACTCAGTGTGG 2

Search completed: October 2, 2001, 16:55:05
Job time: 17668 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: October 2, 2001, 21:50:16 ; Search time 17695.9 Seconds
(without alignments)
16.701 Million cell updates/sec

Title: US-09-757-100B-16

Perfect score: 20

Sequence: 1 ctaggaggaggtcagtggtgg 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 14155048 seqs, 738840595 residues

Total number of hits satisfying chosen parameters: 4519004

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Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

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- 38: /cgn2_6/ptodata/1/pna/US099F_COMB.seq:*
- 39: /cgn2_6/ptodata/1/pna/US099G_COMB.seq:*
- 40: /cgn2_6/ptodata/1/pna/US099H_COMB.seq:*
- 41: /cgn2_6/ptodata/1/pna/US099I_COMB.seq:*
- 42: /cgn2_6/ptodata/1/pna/US099J_COMB.seq:*
- 43: /cgn2_6/ptodata/1/pna/US099K_COMB.seq:*

- 44: /cgn2_6/ptodata/1/pna/US6012_COMB.seq:*
- 45: /cgn2_6/ptodata/1/pna/US6013_COMB.seq:*
- 46: /cgn2_6/ptodata/1/pna/US6014_COMB.seq:*
- 47: /cgn2_6/ptodata/1/pna/US6015_COMB.seq:*
- 48: /cgn2_6/ptodata/1/pna/US6016_COMB.seq:*
- 49: /cgn2_6/ptodata/1/pna/US6017_COMB.seq:*
- 50: /cgn2_6/ptodata/1/pna/US6018_COMB.seq:*
- 51: /cgn2_6/ptodata/1/pna/US6019_COMB.seq:*
- 52: /cgn2_6/ptodata/1/pna/US6020_COMB.seq:*
- 53: /cgn2_6/ptodata/1/pna/US6021_COMB.seq:*
- 54: /cgn2_6/ptodata/1/pna/US6022_COMB.seq:*
- 55: /cgn2_6/ptodata/1/pna/US6023_COMB.seq:*
- 56: /cgn2_6/ptodata/1/pna/US6024_COMB.seq:*
- 57: /cgn2_6/ptodata/1/pna/US6025_COMB.seq:*
- 58: /cgn2_6/ptodata/1/pna/US6026_COMB.seq:*
- 59: /cgn2_6/ptodata/1/pna/US6027_COMB.seq:*
- 60: /cgn2_6/ptodata/1/pna/US6028_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
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2	20	100.0	20	17	US-09-377-310-16
3	20	100.0	20	29	US-09-757-100B-16
4	15	75.0	15	1	PCT-US00-18999-36
5	15	75.0	15	17	US-09-377-310-36
6	15	75.0	15	29	US-09-757-100B-36
7	14.4	72.0	25	26	US-09-660-220-71852
8	14.4	72.0	25	26	US-09-660-220-78149
9	13.8	69.0	25	55	US-60-233-166-385862
10	13.8	69.0	25	55	US-60-233-166-406405
11	13.8	69.0	25	55	US-60-234-017-120917
12	13.8	69.0	25	55	US-60-234-017-120921
13	13.8	69.0	28	1	PCT-US00-26619-18
14	13.6	68.0	25	26	US-09-660-220-94301
15	13.4	67.0	34	7	US-08-305-771A-53
16	13.4	67.0	35	7	US-08-305-771A-57
17	13.2	66.0	18	9	US-08-585-684-2592
18	13.2	66.0	18	9	US-08-585-684A-2592
19	13.2	66.0	20	1	PCT-US99-23205-87
20	13.2	66.0	21	16	US-09-266-682-6
21	13.2	66.0	21	17	US-09-322-134-6
22	13.2	66.0	23	8	US-08-472-801-3446
23	13.2	66.0	23	10	US-08-668-235-3446
24	13.2	66.0	25	55	US-60-233-166-23415
25	13.2	66.0	25	55	US-60-233-166-23416
26	13.2	66.0	25	55	US-60-233-166-3638
27	13.2	66.0	33	1	PCT-US96-03686B-7
28	13.2	66.0	33	12	US-08-816-772-7
29	13.2	66.0	33	16	US-09-245-024-7
30	13.2	66.0	47	8	US-08-475-228-275
31	13.2	66.0	47	8	US-08-482-080-275
32	13.2	66.0	47	17	US-09-354-947-275
33	13.2	66.0	47	40	US-60-082-614-470
34	13.2	66.0	49	14	US-09-009-490A-94
35	13.2	66.0	25	1	PCT-US00-09865-13
36	12.8	64.0	25	21	US-09-548-933-13
37	12.8	64.0	25	26	US-09-660-220-56881
38	12.8	64.0	25	26	US-09-660-220-56888
39	12.8	64.0	25	26	US-09-660-220-100448
40	12.8	64.0	25	55	US-60-233-166-240151
41	12.8	64.0	25	55	US-60-233-166-364161
42	12.8	64.0	25	55	US-60-233-166-406386
43	12.8	64.0	25	55	US-60-233-166-408388
44	12.8	64.0	25	55	US-60-234-017-309445

ALIGNMENTS

RESULT 1
PCT-US00-18999-16
; Sequence 16, Application PC/TUS0018999
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Monia, Brett P.
; APPLICANT: Gaarde, William A.
; APPLICANT: Nero, Pamela S.
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
; FILE REFERENCE: ISPH-0476
; CURRENT APPLICATION NUMBER: PCT/US00/18999
; PRIOR FILING DATE: 2000-07-13
; PRIOR APPLICATION NUMBER: 09/377,310
; PRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
PCT-US00-18999-16

Query Match 100.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ctaggaggagctcagtggtg 20
Db 1 ctaggaggagctcagtggtg 20

RESULT 2
US-09-377-310-16
; Sequence 16, Application US/09377310A
; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P.
; APPLICANT: Gaarde, William A.
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
; FILE REFERENCE: ISPH-0389
; CURRENT APPLICATION NUMBER: US/09/377,310A
; PRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
US-09-377-310-16

Query Match 100.0%; Score 20; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ctaggaggagctcagtggtg 20
Db 1 ctaggaggagctcagtggtg 20

RESULT 3
US-09-757-100B-16
; Sequence 16, Application US/09757100B

; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P.
; APPLICANT: Gaarde, William A.
; APPLICANT: Nero, Pamela S.
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
; FILE REFERENCE: ISPH-0533
; CURRENT APPLICATION NUMBER: US/09/757,100B
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 09/377,310
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/US00/18999
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
US-09-757-100B-16

Query Match 100.0%; Score 20; DB 29; Length 20;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ctaggaggagctcagtggtg 20
Db 1 ctaggaggagctcagtggtg 20

RESULT 4
PCT-US00-18999-36
; Sequence 36, Application PC/TUS0018999
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Monia, Brett P.
; APPLICANT: Gaarde, William A.
; APPLICANT: Nero, Pamela S.
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
; FILE REFERENCE: ISPH-0476
; CURRENT APPLICATION NUMBER: PCT/US00/18999
; CURRENT FILING DATE: 2000-07-13
; PRIOR APPLICATION NUMBER: 09/377,310
; PRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 36
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
PCT-US00-18999-36

Query Match 75.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 agggaggagctcagtg 17
Db 1 agggaggagctcagtg 15

RESULT 5
US-09-377-310-36
; Sequence 36, Application US/09377310A
; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P.

; APPLICANT: Gaarde, William A.
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
; FILE REFERENCE: ISPH-0389
; CURRENT APPLICATION NUMBER: US/09/377,310A
; CURRENT FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 36
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
US-09-377-310-36

Query Match 75.0%; Score 15; DB 17; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 aggggaggtcagtg 17
| | | | | | | | | | | | | | |
Db 1 aggggaggtcagtg 15

RESULT 6
US-09-757-100b-36
; Sequence 36, Application US/09757100B
; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P.
; APPLICANT: Gaarde, William A.
; APPLICANT: Nero, Pamela S.
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
; TITLE OF INVENTION: Expression
; FILE REFERENCE: ISPH-0533
; CURRENT APPLICATION NUMBER: US/09/757,100B
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 09/377,310
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/US00/18999
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 36
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
US-09-757-100b-36

Query Match 75.0%; Score 15; DB 29; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 aggggaggtcagtg 17
| | | | | | | | | | | | | | |
Db 1 aggggaggtcagtg 15

RESULT 7
US-09-660-220-71852
; Sequence 71852, Application US/09660220
; GENERAL INFORMATION:
; APPLICANT: Mittmann et al.
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of Human
; FILE REFERENCE: 3102.1
; CURRENT APPLICATION NUMBER: US/09/660,220
; CURRENT FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 60/164,973

; PRIOR FILING DATE: 1999-11-11
; NUMBER OF SEQ ID NOS: 140981
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 71852
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo Sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank S76992
US-09-660-220-71852

Query Match 72.0%; Score 14.4; DB 26; Length 25;
Best Local Similarity 93.8%; Pred. No. 7.6e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 aggggaggtcagtg 18
| | | | | | | | | | | | | | |
Db 1 aggggaggtcagtg 16

RESULT 8
US-09-660-220-78149/c
; Sequence 78149, Application US/09660220
; GENERAL INFORMATION:
; APPLICANT: Mittmann et al.
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of Human
; FILE REFERENCE: 3102.1
; CURRENT APPLICATION NUMBER: US/09/660,220
; CURRENT FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 60/164,973
; PRIOR FILING DATE: 1999-11-11
; NUMBER OF SEQ ID NOS: 140981
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 78149
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo Sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank U10439
US-09-660-220-78149

Query Match 72.0%; Score 14.4; DB 26; Length 25;
Best Local Similarity 93.8%; Pred. No. 7.6e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 ggggaggtcagtg 19
| | | | | | | | | | | | | | |
Db 20 GGGGAGACTCAGTGTG 5

RESULT 9
US-60-233-166-385862/c
; Sequence 385862, Application US/60233166
; GENERAL INFORMATION:
; APPLICANT: Mittmann
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat
; FILE REFERENCE: 3112
; CURRENT APPLICATION NUMBER: US/60/233,166
; CURRENT FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 420907
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 385862
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: Affymetrix Proprieta
US-60-233-166-385862

Query Match 69.0%; Score 13.8; DB 55; Length 25;
Best Local Similarity 88.2%; Pred. No. 1.5e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ctaggaggagctcagtg 17
||| ||||| |||||
Db 22 CTACGGGAGCTCAGTG 6

RESULT 10
US-60-233-166-406405
; Sequence 406405, Application US/60233166
; GENERAL INFORMATION:
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat
; FILE REFERENCE: 3112
; CURRENT APPLICATION NUMBER: US/60/233,166
; NUMBER OF SEQ ID NOS: 2000-10-24
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 406405
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: Affymetrix Proprieta
US-60-233-166-406405

Query Match 69.0%; Score 13.8; DB 55; Length 25;
Best Local Similarity 88.2%; Pred. No. 1.5e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ctaggaggagctcagtg 17
||| ||||| |||||
Db 6 ctagggaagactcagtg 22

RESULT 11
US-60-234-017-120917
; Sequence 120917, Application US/60234017
; GENERAL INFORMATION:
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of Mus
; FILE REFERENCE: 3115
; CURRENT APPLICATION NUMBER: US/60/234,017
; NUMBER OF SEQ ID NOS: 2000-09-20
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 120917
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank U64445
US-60-234-017-120917

Query Match 69.0%; Score 13.8; DB 55; Length 25;
Best Local Similarity 88.2%; Pred. No. 1.5e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ctaggaggagctcagtg 17
||| ||||| |||||
Db 2 ctagggaagactcagtg 18

RESULT 12
US-60-234-017-120921
; Sequence 120921, Application US/60234017
; GENERAL INFORMATION:
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of Mus
; FILE REFERENCE: 3115
; CURRENT APPLICATION NUMBER: US/60/234,017
; CURRENT FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 605887
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 120921
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank U64445
US-60-234-017-120921

Query Match 69.0%; Score 13.8; DB 55; Length 25;
Best Local Similarity 88.2%; Pred. No. 1.5e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ctaggaggagctcagtg 17
||| ||||| |||||
Db 1 ctagggaagactcagtg 17

RESULT 13
PCT-US00-26619-18
; Sequence 18, Application PC/TUS0026619
; GENERAL INFORMATION:
; APPLICANT: Meares, Claude
; APPLICANT: Chmura, Albert
; TITLE OF INVENTION: The Regents of the University of California
; FILE REFERENCE: 023070-099120PC
; CURRENT APPLICATION NUMBER: PCT/US00/26619
; CURRENT FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US 60/156,194
; PRIOR FILING DATE: 1999-09-27
; PRIOR APPLICATION NUMBER: US 60/208,684
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:cloning primer
; OTHER INFORMATION: with XhoI site
PCT-US00-26619-18

Query Match 69.0%; Score 13.8; DB 1; Length 28;
Best Local Similarity 88.2%; Pred. No. 1.5e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ctaggaggagctcagtg 17
||| ||||| |||||
Db 12 ctgggggagactcagtg 28

RESULT 14
US-09-660-220-94301/c
; Sequence 94301, Application US/09660220
; GENERAL INFORMATION:
; APPLICANT: Mittmann et al.
; APPLICANT: Affymetrix, Inc.

; TITLE OF INVENTION: Methods of Genetic Analysis of Human
; FILE REFERENCE: 3102.1
; CURRENT APPLICATION NUMBER: US/09/660,220
; CURRENT FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 60/164,973
; PRIOR FILING DATE: 1999-11-11
; NUMBER OF SEQ ID NOS: 140981
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 94301
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo Sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank U51003
US-09-660-220-94301

Query Match 68.0%; Score 13.6; DB 26; Length 25;
Best Local Similarity 80.0%; Pred. No. 1.9e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ctaggaggagctcagtgtgg 20
||||||| ||| |||
Db 25 CTAGGGAGGCTCGTGTGG 6

RESULT 15

US-08-305-771A-53
; Sequence 53, Application US/08305771A
; GENERAL INFORMATION:
; APPLICANT: Barbara Sosnowski
; APPLICANT: Lois Chandler
; APPLICANT: L. L. Houston
; APPLICANT: Michael Nova
; TITLE OF INVENTION: CONJUGATES OF HEPARIN-BINDING EPIDERMAL
; TITLE OF INVENTION: GROWTH FACTOR-LIKE GROWTH FACTOR AND TARGETED AGENTS
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/305,771A
; FILING DATE: September 13, 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/297,961
; FILING DATE: 29-AUG-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/213,446
; FILING DATE: 15-MAR-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/213,447
; FILING DATE: 15-MAR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L.
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 519522
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619)238-0999
; TELEFAX: (619)238-0062
; INFORMATION FOR SEQ ID NO: 53:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-305-771A-53

Query Match 67.0%; Score 13.4; DB 7; Length 34;
Best Local Similarity 93.3%; Pred. No. 2.4e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ctaggggagggtcag 15
||||| ||| ||| ||| |||
Db 11 CTATGGGAGGCTCAG 25

Search completed: October 2, 2001, 21:50:17
Job time: 24530 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: October 2, 2001, 16:55:04 ; Search time 2173.58 Seconds
(without alignments)
19.290 Million cell updates/sec

Title: US-09-757-100B-15

Perfect score: 20

Sequence: 1 ttgttggttccaatcgacc 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1895189 seqs, 1048201267 residues

Total number of hits satisfying chosen parameters: 299022

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 2: /cgn2.6/ptodata/2/pna/US06_NEW_COMB.seq.*
- 3: /cgn2.6/ptodata/2/pna/US07_NEW_COMB.seq.*
- 4: /cgn2.6/ptodata/2/pna/US08_NEW_COMB.seq.*
- 5: /cgn2.6/ptodata/2/pna/US09_NEW_COMB.seq.*
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- 8: /cgn2.6/ptodata/2/pna/US60_NEW_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
C 1	13.2	66.0	32	7	US-09-724-671-20856
C 2	12.2	61.0	33	8	US-60-252-833-23017
C 3	12	60.0	20	6	US-09-198-452A-5586
C 4	12	60.0	48	8	US-60-253-653-5980
C 5	11.8	59.0	22	7	US-09-653-971A-4
C 6	11.8	59.0	35	6	US-09-882-246-29
C 7	11.4	57.0	25	5	US-09-623-025A-8
C 8	11.4	57.0	49	8	US-60-253-456-27270
C 9	11.2	56.0	20	6	US-09-198-452A-1694
C 10	11.2	56.0	20	6	US-09-198-452A-4752
C 11	11.2	56.0	38	8	US-60-253-378-10923
C 12	11.2	56.0	40	8	US-60-253-651-7574
C 13	11.2	56.0	50	7	US-09-822-698A-14
C 14	11	55.0	24	7	PCT-US99-05606-8
C 15	11	55.0	17	7	US-09-730-559B-55
C 16	11	55.0	28	8	US-60-253-457-11420
C 17	11	55.0	31	5	US-09-574-376B-736
C 18	11	55.0	44	8	US-60-253-651-24602
C 19	11	55.0	46	8	US-60-253-378-10394
C 20	11	55.0	50	8	US-60-253-457-41965
C 21	10.8	54.0	20	6	US-09-198-452A-2476
C 22	10.8	54.0	26	6	US-09-752-110A-6
C 23	10.8	54.0	28	6	US-09-752-110A-9
C 24	10.8	54.0	35	6	US-09-882-246-27
C 25	10.8	54.0	41	8	US-60-253-654-8477

ALIGNMENTS

RESULT 1

US-09-724-671-20856/c

; Sequence 20856, Application US/09724671

; GENERAL INFORMATION:

; APPLICANT: Watson, James D

; APPLICANT: Murison, James G

; TITLE OF INVENTION: Polynucleotides, polypeptides expressed

; FILE REFERENCE: 105002

; CURRENT APPLICATION NUMBER: US/09724,671

; CURRENT FILING DATE: 2000-11-28

; PRIOR APPLICATION NUMBER: U.S. No. 60/171,678

; NUMBER OF SEQ ID NOS: 21907

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 20856

; LENGTH: 32

; TYPE: DNA

; ORGANISM: Mouse

US-09-724-671-20856

Query Match 66.0%; Score 13.2; DB 7; Length 32;

Best Local Similarity 83.3%; Pred. No. 1.1e+03;

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 ttggtttccaatcgacc 20

DB 32 TCGGCTTCCAATAGGACC 15

RESULT 2

US-60-252-833-23017

; Sequence 23017, Application US/60252833

; GENERAL INFORMATION:

; APPLICANT: Grigor, Murray R

; APPLICANT: Glenn, Matthew

; TITLE OF INVENTION: Compositions isolated from bovine

; FILE REFERENCE: 1052P2

; CURRENT APPLICATION NUMBER: US/60/252,833

; CURRENT FILING DATE: 2000-11-21

; NUMBER OF SEQ ID NOS: 43535

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 23017

; LENGTH: 33

; TYPE: DNA

; ORGANISM: Bovine

Sequence 8477, Ap
Sequence 14850, A
Sequence 1727, Ap
Sequence 3091, Ap
Sequence 2642, Ap
Sequence 2643, Ap
Sequence 46, Appl
Sequence 41, Appl
Sequence 2875, Ap
Sequence 5086, Ap
Sequence 7, Appl
Sequence 1225, Ap
Sequence 256, App
Sequence 256, App
Sequence 7833, Ap
Sequence 7431, Ap
Sequence 7431, Ap
Sequence 15900, A
Sequence 34, Appl

APPLICANT: DUCKWORTH, DAVID MALCOLM

APPLICATION NUMBER: 07/536,428

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;
; FILING DATE: 11 JUNE 1990
; APPLICATION NUMBER: 07/931,473
; FILING DATE: 17 AUGUST 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Barry J. Swanson
; REGISTRATION NUMBER: 33,215
; REFERENCE/DOCKET NUMBER: NEX10/US-CON
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 793-3333
; TELEFAX: (303) 793-3433
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 35 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 29:
US-09-882-246-29

Query Match          59.0%; Score 11.8; DB 6; Length 35;
Best Local Similarity 40.0%; Pred. No. 6.4e+03;
Matches 6; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ttgtggttccaatc 15
   :|::|::|::|::|
Db 18 UGUUGUUGUCCACUC 32

RESULT 7
US-09-623-025A-8/c
; Sequence 8, Application US/09623025A
; GENERAL INFORMATION:
; APPLICANT: University of Nevada-Reno, Richard Bjur, PhD, JD
; TITLE OF INVENTION: Identification of Oxidant Isoform of Human MnSOD
; FILE REFERENCE: unevadareno5013
; CURRENT APPLICATION NUMBER: US/09/623,025A
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: PCT/US99/04129
; PRIOR FILING DATE: 1998-02-25
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 25
; TYPE: DNA
; ORGANISM: oligonucleotide
US-09-623-025A-8

Query Match          57.0%; Score 11.4; DB 6; Length 25;
Best Local Similarity 92.3%; Pred. No. 1e+04;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ttgtggttccaac 13
   ||||| |||||
Db 24 TGTGTGTGTCGAA 12

RESULT 8
US-60-253-456-27270
; Sequence 27270, Application US/60253456
; GENERAL INFORMATION:
; APPLICANT: Havukkala, Ilkka J
; TITLE OF INVENTION: Polynucleotides, isolated from
; FILE REFERENCE: 1054P1
; CURRENT APPLICATION NUMBER: US/60/253,456
; CURRENT FILING DATE: 2000-11-27
; NUMBER OF SEQ ID NOS: 37096
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27270
; LENGTH: 49
; TYPE: DNA
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;
; ORGANISM: Pinus radiata
US-60-253-456-27270

Query Match          57.0%; Score 11.4; DB 8; Length 49;
Best Local Similarity 92.3%; Pred. No. 1.1e+04;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 ttggtttccaatc 15
   ||||| |||||
Db 1 ttggtttccaatc 13

RESULT 9
US-09-198-452A-1694/c
; Sequence 1694, Application US/09198452A
; GENERAL INFORMATION:
; APPLICANT: Griffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragme
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, pr
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 1694
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-1694

Query Match          56.0%; Score 11.2; DB 6; Length 20;
Best Local Similarity 81.2%; Pred. No. 1.3e+04;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 ggtttccaatcgacc 20
   ||||| |||||
Db 19 GGTttCCAATTGCCC 4

RESULT 10
US-09-198-452A-4752/c
; Sequence 4752, Application US/09198452A
; GENERAL INFORMATION:
; APPLICANT: Griffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragme
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, pr
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 4752
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-4752

Query Match          56.0%; Score 11.2; DB 6; Length 20;
Best Local Similarity 81.2%; Pred. No. 1.3e+04;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 gttggtttccaatcgg 17
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Db 17 GTTGGATACAAATCGG 2

RESULT 11
US-60-253-378-10923
; Sequence 10923, Application US/60253378
; GENERAL INFORMATION:
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; APPLICANT: Havukkala, Ilkka J
; TITLE OF INVENTION: Polynucleotides isolated from plants
; FILE REFERENCE: 1054P3
; CURRENT APPLICATION NUMBER: US/60/253,378
; CURRENT FILING DATE: 2000-11-27
; NUMBER OF SEQ ID NOS: 40367
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10923
; LENGTH: 38
; TYPE: DNA
; ORGANISM: Pinus radiata
US-60-253-378-10923

Query Match 56.0%; Score 11.2; DB 8; Length 38;
Best Local Similarity 81.2%; Pred. No. 1.4e+04;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ttgtgtttcccaatcg 16
||| ||||| ||
Db 19 ttgtgtttccctagcg 34

RESULT 12

US-60-253-651-7574
; Sequence 7574, Application US/60253651
; GENERAL INFORMATION:

; APPLICANT: Glenn, Matthew
; APPLICANT: Grigor, Murray R
; TITLE OF INVENTION: Compositions isolated from bovine tissue
; FILE REFERENCE: 1055P3
; CURRENT APPLICATION NUMBER: US/60/253,651
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 27858
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7574
; LENGTH: 40
; TYPE: DNA
; ORGANISM: Bovine
US-60-253-651-7574

Query Match 56.0%; Score 11.2; DB 8; Length 40;
Best Local Similarity 81.2%; Pred. No. 1.4e+04;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 ttgtgtttcccaatcgga 18
||| ||||| ||||
Db 25 ttgactttccaaacgga 40

RESULT 13

US-09-822-698A-14/c

; Sequence 14, Application US/09822698A
; GENERAL INFORMATION:

; APPLICANT: Hendrickx, Maria P.G.
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYA-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 14
; LENGTH: 50
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: VL forward primer for light chain variable region

; OTHER INFORMATION: of PHI Fab antibody with additional linker and
; OTHER INFORMATION: restriction sites
US-09-822-698A-14

Query Match 56.0%; Score 11.2; DB 7; Length 50;
Best Local Similarity 81.2%; Pred. No. 1.5e+04;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 gttggtttcccaatcg 17
||| ||||| ||||
Db 32 GTGGATATCCAATCGG 17

RESULT 14

PCT-US99-05606-8

; Sequence 8, Application PC/TUS9905606
; GENERAL INFORMATION:
; APPLICANT: Millentum Pharmaceuticals, Inc.
; APPLICANT: Regents of the University of California
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND TREATING CHROMOSOME-18p RELATED DISORDERS
; FILE REFERENCE: 7853-138-228
; CURRENT APPLICATION NUMBER: PCT/US99/05606
; CURRENT FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 09/236,134
; PRIOR FILING DATE: 1999-01-22
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
PCT-US99-05606-8

Query Match 55.0%; Score 11; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.6e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 gttggtttccca 12
||| ||||| ||||
Db 5 gttggtttccca 15

RESULT 15

US-09-730-559B-55

; Sequence 55, Application US/09730559B
; GENERAL INFORMATION:

; APPLICANT: ISHIWATA, TETSUYOSHI
; APPLICANT: SAKURADA, MIKIO
; APPLICANT: KAWABATA, AYAKO
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: NISHI, TATSUNARI
; APPLICANT: KUGA, TETSURO
; APPLICANT: SAWADA, SHIGEMASA
; APPLICANT: TAKEI, MASAMI
; APPLICANT: SHIBATA, KENJI
; APPLICANT: FURUYA, AKIO
; TITLE OF INVENTION: Iga NEPHROPATHY-ASSOCIATED GENE
; FILE REFERENCE: 766.21 CIP
; CURRENT APPLICATION NUMBER: US/09/730,559B
; CURRENT FILING DATE: 2000-12-07
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 55
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA

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||| ||| ||| ||| |||
Db 3 t g a t g c t t t t c t a t c t g a c 21

Search completed: October 2, 2001, 16:55:04
Job time: 17667 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: October 2, 2001, 21:50:15 ; Search time 17695.9 Seconds
(without alignments)
16.701 Million cell updates/sec

Title: US-09-757-100B-15
Perfect score: 20
Sequence: 1 tgttggttccaatcgacc 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 14155048 seqs, 7388405095 residues
Total number of hits satisfying chosen parameters: 4519004

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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60: /cgn2_6/ptodata/1/pna/US06028_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	20	100.0	20	1	PCT-US00-18999-15	Sequence 15, Appl
2	20	100.0	20	17	US-09-377-310-15	Sequence 15, Appl
3	20	100.0	20	29	US-09-757-100B-15	Sequence 15, Appl
C 4	15.8	79.0	25	55	US-60-234-017-154082	Sequence 154082,
C 5	15.2	76.0	25	55	US-60-233-620-7572	Sequence 7572, Ap
C 6	15.2	76.0	25	55	US-60-234-017-201094	Sequence 201094,
7	15	75.0	15	1	PCT-US00-18999-35	Sequence 35, Appl
8	15	75.0	15	17	US-09-377-310-35	Sequence 35, Appl
9	15	75.0	15	29	US-09-757-100B-35	Sequence 35, Appl
C 10	14.2	71.0	25	55	US-60-233-620-1645	Sequence 1645, Ap
C 11	14.2	71.0	25	55	US-60-234-017-42731	Sequence 42731, A
C 12	14.2	71.0	25	55	US-60-234-017-42735	Sequence 42735, A
C 13	14.2	71.0	25	55	US-60-234-017-196005	Sequence 196005,
C 14	14.2	71.0	25	55	US-60-234-017-216701	Sequence 216701,
C 15	13.8	69.0	25	55	US-60-232-638-33957	Sequence 33957, A
C 16	13.8	69.0	25	55	US-60-233-166-79738	Sequence 79738, A
C 17	13.8	69.0	25	55	US-09-404-520-38668	Sequence 38668, A
C 18	13.6	68.0	25	26	US-09-660-220-65925	Sequence 65925, A
C 19	13.6	68.0	25	55	US-60-232-638-137242	Sequence 137242,
C 20	13.6	68.0	25	55	US-60-233-166-184627	Sequence 184627,
C 21	13.6	68.0	46	13	US-08-983-474-6	Sequence 6, Appl
C 22	13.6	68.0	46	13	US-08-983-474A-6	Sequence 6, Appl
C 23	13.4	67.0	25	55	US-60-234-017-261020	Sequence 261020,
C 24	13.2	66.0	25	55	US-60-232-638-69603	Sequence 69603, A
C 25	13.2	66.0	25	55	US-60-232-638-131648	Sequence 131648,
C 26	13.2	66.0	25	55	US-60-232-638-131659	Sequence 131659,
C 27	13.2	66.0	25	55	US-60-233-166-258281	Sequence 258281,
C 28	13.2	66.0	25	55	US-60-233-166-266921	Sequence 266921,
C 29	13.2	66.0	25	55	US-60-233-166-408428	Sequence 408428,
C 30	13.2	66.0	25	55	US-60-234-017-167542	Sequence 167542,
C 31	13.2	66.0	25	55	US-60-234-017-209729	Sequence 209729,
C 32	13.2	66.0	25	55	US-60-234-017-275344	Sequence 275344,
C 33	13.2	66.0	25	55	US-60-234-017-476537	Sequence 476537,
C 34	13.2	66.0	25	55	US-60-234-049-30000	Sequence 30000, A
C 35	13.2	66.0	26	10	US-08-624-655A-6	Sequence 6, Appl
C 36	13.2	66.0	47	18	US-09-422-978-3652	Sequence 3652, Ap
C 37	13	65.0	25	55	US-60-233-620-122282	Sequence 122282,
C 38	13	65.0	25	55	US-60-234-017-218413	Sequence 218413,
C 39	13	65.0	25	55	US-60-234-017-218414	Sequence 218414,
C 40	12.8	64.0	18	28	US-09-422-978-5568	Sequence 5568, Ap
C 41	12.8	64.0	20	18	US-09-703-708-17795	Sequence 17795, A
C 42	12.8	64.0	20	48	US-60-164-320-17795	Sequence 17795, A
C 43	12.8	64.0	20	50	US-60-183-791-17795	Sequence 17795, A
C 44	12.8	64.0	25	26	US-09-660-220-34480	Sequence 34480, A
C 45	12.8	64.0	25	55	US-60-234-049-84625	Sequence 84625, A

ALIGNMENTS

RESULT 1
PCT-US00-18999-15
; Sequence 15, Application PC/TUS0018999
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Monia, Brett P.
; APPLICANT: Gaarde, William A.
; APPLICANT: Nero, Pamela S.
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
; FILE REFERENCE: ISPH-0476
; CURRENT APPLICATION NUMBER: PCT/US00/18999
; PRIOR FILING DATE: 2000-07-13
; PRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
PCT-US00-18999-15

Query Match 100.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tgggtgttccaatcgacc 20
|||||
Db 1 tgggtgttccaatcgacc 20

RESULT 2
US-09-377-310-15
; Sequence 15, Application US/09377310A
; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P.
; APPLICANT: Gaarde, William A.
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
; FILE REFERENCE: ISPH-0389
; CURRENT APPLICATION NUMBER: US/09/377,310A
; PRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
US-09-377-310-15

Query Match 100.0%; Score 20; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tgggtgttccaatcgacc 20
|||||
Db 1 tgggtgttccaatcgacc 20

RESULT 3
US-09-757-100B-15
; Sequence 15, Application US/09757100B

; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P.
; APPLICANT: Gaarde, William A.
; APPLICANT: Nero, Pamela S.
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
; FILE REFERENCE: ISPH-0533
; CURRENT APPLICATION NUMBER: US/09/757,100B
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 09/377,310
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/US00/18999
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
US-09-757-100B-15

Query Match 100.0%; Score 20; DB 29; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tgggtgttccaatcgacc 20
|||||
Db 1 tgggtgttccaatcgacc 20

RESULT 4
US-60-234-017-154082/c
; Sequence 154082, Application US/60234017
; GENERAL INFORMATION:
; APPLICANT: Mitmann, M
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of Mus
; FILE REFERENCE: 3115
; CURRENT APPLICATION NUMBER: US/60/234,017
; CURRENT FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 605887
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 154082
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank AI854607
US-60-234-017-154082

Query Match 79.0%; Score 15.8; DB 55; Length 25;
Best Local Similarity 89.5%; Pred. No. 4.7e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tgggtgttccaatcgacc 19
|||||
Db 19 TGTGTTTCAATCGAAC 1

RESULT 5
US-60-233-620-7572/c
; Sequence 7572, Application US/60233620
; GENERAL INFORMATION:
; APPLICANT: Mitmann
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of
; FILE REFERENCE: 3116
US-60-233-620-7572/c

; CURRENT APPLICATION NUMBER: US/60/233,620
; CURRENT FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 131820
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7572
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank AC003028
US-60-233-620-7572

Query Match 76.0%; Score 15.2; DB 55; Length 25;
Best Local Similarity 85.0%; Pred. No. 9.8e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ttgtgtttccaatcgacc 20
Db 25 TCTTGGTTTCCACTCCGACC 6

RESULT 6
US-60-234-017-201094/c
; Sequence 201094, Application US/60234017
; GENERAL INFORMATION:
; APPLICANT: Mittmann, M
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of Mus
; FILE REFERENCE: 3115
; CURRENT APPLICATION NUMBER: US/60/234,017
; CURRENT FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 605887
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 201094
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank AA792731
US-60-234-017-201094

Query Match 76.0%; Score 15.2; DB 55; Length 25;
Best Local Similarity 85.0%; Pred. No. 9.8e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ttgtgtttccaatcgacc 20
Db 25 TGTGTGTTATCCACGCGACC 6

RESULT 7
PCT-US00-18999-35
; Sequence 35, Application PC/TUS0018999
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Monia, Brett P.
; APPLICANT: Gaarde, William A.
; APPLICANT: Nero, Pamela S.
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
; FILE REFERENCE: ISPH-0476
; CURRENT APPLICATION NUMBER: PCT/US00/18999
; CURRENT FILING DATE: 2000-07-13
; PRIOR APPLICATION NUMBER: 09/377,310
; PRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 35
; LENGTH: 15
; TYPE: DNA

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
PCT-US00-18999-35

Query Match 75.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ttggtttccaatcg 17
Db 1 ttggtttccaatcg 15

RESULT 8
US-09-377-310-35
; Sequence 35, Application US/09377310A
; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P.
; APPLICANT: Gaarde, William A.
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
; FILE REFERENCE: ISPH-0389
; CURRENT APPLICATION NUMBER: US/09/377,310A
; CURRENT FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 35
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
US-09-377-310-35

Query Match 75.0%; Score 15; DB 17; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ttggtttccaatcg 17
Db 1 ttggtttccaatcg 15

RESULT 9
US-09-757-100B-35
; Sequence 35, Application US/09757100B
; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P.
; APPLICANT: Gaarde, William A.
; APPLICANT: Nero, Pamela S.
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
; FILE REFERENCE: ISPH-0533
; CURRENT APPLICATION NUMBER: US/09/757,100B
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 09/377,310
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/US00/18999
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 35
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
US-09-757-100B-35

Query Match 75.0%; Score 15; DB 29; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 ttgggtttccaatcgg 17
||||| ||||| |||||

Db 1 ttgggtttccaatcgg 15

RESULT 10

US-60-233-620-1645/c

; Sequence 1645, Application US/60233620

; GENERAL INFORMATION:

; APPLICANT: Mittmann

; APPLICANT: Affymetrix, Inc.

; TITLE OF INVENTION: Methods of Genetic Analysis of

; FILE REFERENCE: 3116

; CURRENT APPLICATION NUMBER: US/60/233,620

; CURRENT FILING DATE: 2000-10-24

; NUMBER OF SEQ ID NOS: 131820

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 1645

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Arabidopsis thaliana

; PUBLICATION INFORMATION:

; DATABASE ACCESSION NUMBER: GenBank AC000132

US-60-233-620-1645

Query Match 71.0%; Score 14.2; DB 55; Length 25;
Best Local Similarity 84.2%; Pred. No. 3.4e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 gttggtttccaatcgacc 20
||||| ||||| |||||

Db 23 GTTCGTTACCAATAGGACC 5

RESULT 11

US-60-234-017-42731/c

; Sequence 42731, Application US/60234017

; GENERAL INFORMATION:

; APPLICANT: Mittmann, M

; APPLICANT: Affymetrix, Inc.

; TITLE OF INVENTION: Methods of Genetic Analysis of Mus

; FILE REFERENCE: 3115

; CURRENT APPLICATION NUMBER: US/60/234,017

; CURRENT FILING DATE: 2000-09-20

; NUMBER OF SEQ ID NOS: 605887

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 42731

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Mus musculus

; PUBLICATION INFORMATION:

; DATABASE ACCESSION NUMBER: GenBank L03215

US-60-234-017-42731

Query Match 71.0%; Score 14.2; DB 55; Length 25;
Best Local Similarity 84.2%; Pred. No. 3.4e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 gttggtttccaatcgacc 20
||||| ||||| |||||

Db 23 GTTCGTTACCAATAGGACC 5

RESULT 12

US-60-234-017-42735/c

; Sequence 42735, Application US/60234017

; GENERAL INFORMATION:

; APPLICANT: Mittmann, M

; APPLICANT: Affymetrix, Inc.

; TITLE OF INVENTION: Methods of Genetic Analysis of Mus

; FILE REFERENCE: 3115

; CURRENT APPLICATION NUMBER: US/60/234,017

; CURRENT FILING DATE: 2000-09-20

; NUMBER OF SEQ ID NOS: 605887

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 42735

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Mus musculus

; PUBLICATION INFORMATION:

; DATABASE ACCESSION NUMBER: GenBank L03215

US-60-234-017-42735

Query Match 71.0%; Score 14.2; DB 55; Length 25;
Best Local Similarity 84.2%; Pred. No. 3.4e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 gttggtttccaatcgacc 20
||||| ||||| |||||

Db 19 GTTCGTTCCCGATCGGACC 1

RESULT 13

US-60-234-017-196005/c

; Sequence 196005, Application US/60234017

; GENERAL INFORMATION:

; APPLICANT: Mittmann, M

; APPLICANT: Affymetrix, Inc.

; TITLE OF INVENTION: Methods of Genetic Analysis of Mus

; FILE REFERENCE: 3115

; CURRENT APPLICATION NUMBER: US/60/234,017

; CURRENT FILING DATE: 2000-09-20

; NUMBER OF SEQ ID NOS: 605887

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 196005

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Mus musculus

; PUBLICATION INFORMATION:

; DATABASE ACCESSION NUMBER: GenBank AAL75641

US-60-234-017-196005

Query Match 71.0%; Score 14.2; DB 55; Length 25;
Best Local Similarity 84.2%; Pred. No. 3.4e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 gttggtttccaatcgacc 20
||||| ||||| |||||

Db 25 GTTCGTTCCCGATCGGATC 7

RESULT 14

US-60-234-017-216701

; Sequence 216701, Application US/60234017

; GENERAL INFORMATION:

; APPLICANT: Mittmann, M

; APPLICANT: Affymetrix, Inc.

; TITLE OF INVENTION: Methods of Genetic Analysis of Mus

; FILE REFERENCE: 3115

; CURRENT APPLICATION NUMBER: US/60/234,017

; CURRENT FILING DATE: 2000-09-20

; NUMBER OF SEQ ID NOS: 605887

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 216701

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Mus musculus

; PUBLICATION INFORMATION:

; DATABASE ACCESSION NUMBER: GenBank AAL75641

; SEQ ID NO 216701
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank AY789319
US-60-234-017-216701

Query Match 71.0%; Score 14.2; DB 55; Length 25;
Best Local Similarity 84.2%; Pred. No. 3.4e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2 ttgtgtttccaatcgacc 20
||||||| | ||||| |
Db 1 ttgtgtttacgatcggtcc 19

RESULT 15
US-60-232-638-33957/c
; Sequence 33957; Application US/60232638
; GENERAL INFORMATION:
; APPLICANT: Mittmann
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of Yeast
; FILE REFERENCE: 3110
; CURRENT APPLICATION NUMBER: US/60/232,638
; CURRENT FILING DATE: 2000-09-14
; NUMBER OF SEQ ID NOS: 138410
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33957
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: SGD YBR001C
US-60-232-638-33957

Query Match 69.0%; Score 13.8; DB 55; Length 25;
Best Local Similarity 88.2%; Pred. No. 5.5e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 4 ttgtttccaatcgacc 20
||||||| | ||||| |
Db 20 TGGTTTATATCGGACC 4

Search completed: October 2, 2001, 21:50:16
Job time: 24529 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: October 2, 2001, 16:55:03 ; Search time 2173.58 Seconds
(without alignments)
19,290 Million cell updates/sec

Title: US-09-757-100B-14

Perfect score: 20.

Sequence: 1 ggttagggatggtgcgctca 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1895189 seqs, 1048201267 residues

Total number of hits satisfying chosen parameters: 295022

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Pending_Patents_NA_New.*

1: /cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq.*
2: /cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq.*
3: /cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq.*
4: /cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq.*
5: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq.*
6: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq1.*
7: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq2.*
8: /cgn2_6/ptodata/2/pna/US60_NEW_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
c 1	12.6	63.0	32	7	US-09-735-271-1541
c 2	12.6	63.0	33	7	US-09-672-217-151
c 3	12.6	63.0	33	7	US-09-672-217-253
c 4	12.6	63.0	37	5	US-09-536-784-339
c 5	12.6	63.0	37	6	US-09-765-272-339
c 6	12.4	62.0	31	5	US-09-574-376B-1253
c 7	12.2	61.0	21	6	US-09-715-849-504
c 8	12.0	60.0	38	5	US-09-371-772B-7196
c 9	12.0	60.0	38	5	US-09-371-772B-10090
c 10	12.0	60.0	38	5	US-09-708-690-9473
c 11	12.0	60.0	38	5	US-09-708-690-12367
c 12	11.8	59.0	31	7	US-09-840-424-947
c 13	11.8	59.0	33	7	US-09-908-744-61
c 14	11.6	58.0	26	8	US-60-253-654-14371
c 15	11.6	58.0	26	8	US-60-255-592-14371
c 16	11.4	57.0	19	6	US-09-375-318-65
c 17	11.4	57.0	21	6	US-09-508-891-1
c 18	11.4	57.0	45	7	US-09-908-827-27
c 19	11.2	56.0	43	8	US-60-253-651-1558
c 20	11.0	55.0	30	7	US-09-890-997-3
c 21	11.0	55.0	32	6	US-09-787-097-5
c 22	11.0	55.0	36	5	US-09-274-553C-1747
c 23	11.0	55.0	36	5	US-09-406-643-1833
c 24	11.0	55.0	37	6	US-09-546-745A-7011
c 25	11.0	55.0	37	7	US-09-735-271-1542

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26 11 55.0 38 5 US-09-371-772B-7552 Sequence 7552, Ap
27 11 55.0 38 5 US-09-371-772B-8141 Sequence 8141, Ap
28 11 55.0 38 5 US-09-371-772B-9645 Sequence 9645, Ap
29 11 55.0 38 5 US-09-371-772B-10487 Sequence 10487, A
30 11 55.0 38 5 US-09-371-772B-10818 Sequence 10818, A
31 11 55.0 38 5 US-09-371-772B-10877 Sequence 10877, A
32 11 55.0 38 5 US-09-371-772B-11311 Sequence 11311, A
33 11 55.0 38 5 US-09-371-772B-11364 Sequence 11364, A
34 11 55.0 38 5 US-09-371-772B-12297 Sequence 12297, A
35 11 55.0 38 5 US-09-371-772B-12605 Sequence 12605, A
36 11 55.0 38 5 US-09-371-772B-13335 Sequence 13335, A
37 11 55.0 38 5 US-09-708-690-9829 Sequence 9829, Ap
38 11 55.0 38 5 US-09-708-690-10418 Sequence 10418, A
39 11 55.0 38 5 US-09-708-690-11922 Sequence 11922, A
40 11 55.0 38 5 US-09-708-690-12764 Sequence 12764, A
41 11 55.0 38 5 US-09-708-690-13095 Sequence 13095, A
42 11 55.0 38 5 US-09-708-690-13154 Sequence 13154, A
43 11 55.0 38 5 US-09-708-690-13588 Sequence 13588, A
44 11 55.0 38 5 US-09-708-690-13641 Sequence 13641, A
45 11 55.0 38 5 US-09-708-690-14574 Sequence 14574, A

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ALIGNMENTS

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RESULT 1
US-09-735-271-1541/c
; Sequence 1541, Application US/09735271
; GENERAL INFORMATION:
; APPLICANT: Daly, Mark J.
; APPLICANT: Hudson, Thomas J.
; APPLICANT: Lander, Eric S.
; APPLICANT: Rioux, John
; APPLICANT: Siminovich, Kathy
; TITLE OF INVENTION: IBD-RELATED POLYMORPHISMS
; FILE REFERENCE: 2825.1025-002
; CURRENT APPLICATION NUMBER: US/09/735,271
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 60/170,257
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 60/196,046
; PRIOR FILING DATE: 2000-04-10
; NUMBER OF SEQ ID NOS: 2058
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1541
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(32)
; OTHER INFORMATION: n = A,T,C or G
US-09-735-271-1541

Query Match 63.0%; Score 12.6; DB 7; Length 32;
Best Local Similarity 75.0%; Pred. No. 4.4e+03;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 ggttagggatggtgcgctca 20
   ||| ||| ||| ||| |||
Db 22 GGTANGGACGGTGGCATCA 3

RESULT 2
US-09-672-217-151
; Sequence 151, Application US/09672217
; GENERAL INFORMATION:
; APPLICANT: FELL, JACK
; APPLICANT: DIAZ, MARA
; APPLICANT: MCCABE, MEADE
; TITLE OF INVENTION: METHOD OF IDENTIFYING PATHOGENIC CRYPTOCOCCI
; FILE REFERENCE: 086222/0143

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; CURRENT APPLICATION NUMBER: US/09/672,217
; CURRENT FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/156,598
; PRIOR FILING DATE: 1999-09-29
; NUMBER OF SEQ ID NOS: 301
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 151
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer/Probe
; US-09-672-217-151

Query Match          63.0%; Score 12.6; DB 7; Length 33;
Best Local Similarity 78.9%; Pred. No. 4.4e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 gttaggatggtgcgtca 20
   ||| ||| ||| ||| |||
Db 15 gttggtgaaggtgcagtca 33

RESULT 3
US-09-672-217-253
; Sequence 253, Application US/09672217
; GENERAL INFORMATION:
; APPLICANT: FELL, JACK
; APPLICANT: DIAZ, MARA
; APPLICANT: MCCABE, MEADE
; TITLE OF INVENTION: METHOD OF IDENTIFYING PATHOGENIC CRYPTOCOCCI
; FILE REFERENCE: 086222/0143
; CURRENT APPLICATION NUMBER: US/09/672,217
; CURRENT FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/156,598
; PRIOR FILING DATE: 1999-09-29
; NUMBER OF SEQ ID NOS: 301
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 253
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer/Probe
; US-09-672-217-253

Query Match          63.0%; Score 12.6; DB 7; Length 33;
Best Local Similarity 78.9%; Pred. No. 4.4e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 gttaggatggtgcgtca 20
   ||| ||| ||| ||| |||
Db 15 gttggtgaaggtgcagtca 33

RESULT 4
US-09-536-784-339/c
; Sequence 339, Application US/09536784
; GENERAL INFORMATION:
; APPLICANT: Choi et. al.
; TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
; NUMBER OF SEQUENCES: 452
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/765,272
; FILING DATE: 22-Jan-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/961,083
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB340P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 339:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 37 base pairs
; TYPE: nucleic acid

```

```

; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/536,784
; FILING DATE: 30-Oct-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/961,083
; FILING DATE: OCT-30-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Michelle S. Marks
; REGISTRATION NUMBER: 41,971
; REFERENCE/DOCKET NUMBER: PB340P3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 339:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 37 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 339:
; US-09-536-784-339

Query Match          63.0%; Score 12.6; DB 5; Length 37;
Best Local Similarity 78.9%; Pred. No. 4.5e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 gttaggatggtgcgtca 20
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Db 19 GCTAGCGATGGATCCGTCA 1

RESULT 5
US-09-765-272-339/c
; Sequence 339, Application US/09765272
; GENERAL INFORMATION:
; APPLICANT: Choi et. al.
; TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
; NUMBER OF SEQUENCES: 452
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/765,272
; FILING DATE: 22-Jan-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/961,083
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB340P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 339:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 37 base pairs
; TYPE: nucleic acid

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STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 339;
US-09-765-272-339

Query Match 63.0%; Score 12.6; DB 6; Length 37;
Best Local Similarity 78.9%; Pred. No. 4.5e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 gttaggatggtgcgtca 20
||| ||||| |||||
DB 19 GCTAGGATGGATCCGTCA 1

RESULT 6
US-09-574-376B-1253/c
; Sequence 1253, Application US/09574376B
; GENERAL INFORMATION:
; APPLICANT: Warrington, Janet
; APPLICANT: Shah, Nila
; APPLICANT: Gingeras, Thomas Raymond
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Human Lymphoblast Polymorphisms
; FILE REFERENCE: 3229.2
; CURRENT APPLICATION NUMBER: US/09/574, 376B
; CURRENT FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 1330
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1253
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
US-09-574-376B-1253

Query Match 62.0%; Score 12.4; DB 5; Length 31;
Best Local Similarity 81.2%; Pred. No. 5.6e+03;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 ttaggatggtgcgt 18
||| ||||| |||||
DB 27 TTGGGGATGGARCCGT 12

RESULT 7
US-09-715-849-504/c
; Sequence 504, Application US/09715849
; GENERAL INFORMATION:
; APPLICANT: Cargill, Michele
; APPLICANT: Ireland, James S.
; APPLICANT: Lander, Eric S.
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: 2825.2002-001
; CURRENT APPLICATION NUMBER: US/09/715, 849
; CURRENT FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: US 60/167, 334
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 589
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 504
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-715-849-504

Query Match 61.0%; Score 12.2; DB 6; Length 21;
Best Local Similarity 73.7%; Pred. No. 6.8e+03;
Matches 14; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 ggttagggatggtgcgtc 19

DB 19 GGTGAGGGMGGTGCAGGC 1
||| ||||| ||||| |||

RESULT 8
US-09-371-772B-7196
; Sequence 7196, Application US/09371772B
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions
; FILE REFERENCE: MBHB00, 876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371, 772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005, 974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584, 040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7196
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-371-772B-7196

Query Match 60.0%; Score 12; DB 5; Length 38;
Best Local Similarity 55.0%; Pred. No. 9.3e+03;
Matches 11; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 ggttagggatggtgcgtca 20
||| ||||| ||||| |||
DB 4 gguacugaugagcgcuua 23

RESULT 9
US-09-371-772B-10090
; Sequence 10090, Application US/09371772B
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions
; FILE REFERENCE: MBHB00, 876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371, 772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005, 974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584, 040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10090
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-371-772B-10090

Query Match 60.0%; Score 12; DB 5; Length 38;
Best Local Similarity 55.0%; Pred. No. 9.3e+03;

Matches 11; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 ggttagggatggtgccgtca 20
||:| ||:| ||||:|
Db 4 gguuacugaugagggccguua 23

RESULT 10

US-09-708-690-9473
; Sequence 9473, Application US/09708690
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00,876-L (400/002)
; CURRENT APPLICATION NUMBER: US/09/708,690
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; PRIOR APPLICATION NUMBER: US 09/371,772
; PRIOR FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 09/685,664
; PRIOR FILING DATE: 2000-10-10
; NUMBER OF SEQ ID NOS: 20828
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9473
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-708-690-9473

Query Match 60.0%; Score 12; DB 5; Length 38;
Best Local Similarity 55.0%; Pred. No. 9.3e+03;
Matches 11; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 ggttagggatggtgccgtca 20
||:| ||:| ||||:|
Db 4 gguuacugaugagggccguua 23

RESULT 11

US-09-708-690-12367
; Sequence 12367, Application US/09708690
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00,876-L (400/002)
; CURRENT APPLICATION NUMBER: US/09/708,690
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; PRIOR APPLICATION NUMBER: US 09/371,772
; PRIOR FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 09/685,664
; PRIOR FILING DATE: 2000-10-10
; NUMBER OF SEQ ID NOS: 20828
; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 12367
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-708-690-12367

Query Match 60.0%; Score 12; DB 5; Length 38;
Best Local Similarity 55.0%; Pred. No. 9.3e+03;
Matches 11; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 ggttagggatggtgccgtca 20
||:| ||:| ||||:|
Db 4 gguuacugaugagggccguua 23

RESULT 12

US-09-840-424-947
; Sequence 947, Application US/09840424
; GENERAL INFORMATION:
; APPLICANT: Gearing, David P.
; APPLICANT: McCarthy, Sean A.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES DERIVED FROM A
; TITLE OF INVENTION: HUMAN MICROVASCULAR ENDOTHELIAL LIBRARY
; FILE REFERENCE: 1600,1010-002
; CURRENT APPLICATION NUMBER: US/09/840,424
; CURRENT FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: US 60/084,098
; PRIOR FILING DATE: 1998-05-04
; PRIOR APPLICATION NUMBER: US 60/123,523
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: US 60/126,974
; PRIOR FILING DATE: 1999-03-30
; PRIOR APPLICATION NUMBER: US 09/304,649
; PRIOR FILING DATE: 1999-05-04
; NUMBER OF SEQ ID NOS: 1311
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 947
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(31)
; OTHER INFORMATION: n = A,T,C or G
US-09-840-424-947

Query Match 59.0%; Score 11.8; DB 7; Length 31;
Best Local Similarity 81.2%; Pred. No. 1.2e+04;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 tagggatggtgccgtc 19
|| | ||||| |||
Db 3 taagnatggtgctgc 18

RESULT 13

US-09-908-744-61
; Sequence 61, Application US/09908744
; GENERAL INFORMATION:
; APPLICANT: Miasnikov Andrei
; APPLICANT: Ojamo Heikki
; APPLICANT: Povelainen Mira
; APPLICANT: Gros H+kan
; APPLICANT: Toivari Mervi
; APPLICANT: Richard Peter
; APPLICANT: Ruohonen Laura
; APPLICANT: Koivuranta Kari
; APPLICANT: Londesborough John
; APPLICANT: Aristidou Aristos

```
; APPLICANT: Penttil, Merja
; APPLICANT: Plazanet-Menut Claire
; APPLICANT: Deutscher Josef
; TITLE OF INVENTION: Manufacture of Five-Carbon Sugars and Sugar Alcohols
; FILE REFERENCE: 1427.0010005
; CURRENT APPLICATION NUMBER: US/09/908,744
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: PCT/FI01/00051
; PRIOR FILING DATE: 2001-01-22
; PRIOR APPLICATION NUMBER: US 09/488,581
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 08/790,585
; PRIOR FILING DATE: 1997-01-29
; PRIOR APPLICATION NUMBER: US 08/368,395
; PRIOR FILING DATE: 1995-01-03
; PRIOR APPLICATION NUMBER: US 08/110,672
; PRIOR FILING DATE: 1993-08-24
; PRIOR APPLICATION NUMBER: US 07/973,325
; PRIOR FILING DATE: 1992-11-05
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 3.0
; SEQ ID NO 61
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: OGDH3 primer
US-09-908-744-61
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Query Match 59.0%; Score 11.8; DB 7; Length 33;
Best Local Similarity 86.7%; Pred. NO. 1.2e+04;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 agggatggtgcgcgc 19
|| ||||| |||
Db 19 agcgatggtgctgc 33
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RESULT 14
US-60-253-654-14371/c
; Sequence 14371, Application US/60253654
; GENERAL INFORMATION:
; APPLICANT: Glenn, Matthew
; APPLICANT: Norriss, Michael G.
; TITLE OF INVENTION: Compositions isolated from forage
; TITLE OF INVENTION: grasses and methods for their use.
; FILE REFERENCE: 1056P
; CURRENT APPLICATION NUMBER: US/60/253,654
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 32581
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14371
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Festuca arundinaceae
US-60-253-654-14371
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Query Match 58.0%; Score 11.6; DB 8; Length 26;
Best Local Similarity 77.8%; Pred. NO. 1.4e+04;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 ttaggatggtgcgcgc 20
|| ||||| |||
Db 18 TTTTGGATGGTTCGGTCA 1
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RESULT 15
US-60-255-592-14371/c
; Sequence 14371, Application US/60255592
; GENERAL INFORMATION:
; APPLICANT: Glenn, Matthew
```

```
; APPLICANT: Norriss, Michael G.
; TITLE OF INVENTION: Compositions isolated from forage
; FILE REFERENCE: 1056P2
; CURRENT APPLICATION NUMBER: US/60/255,592
; CURRENT FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 32581
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14371
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Festuca arundinaceae
US-60-255-592-14371

Query Match 58.0%; Score 11.6; DB 8; Length 26;
Best Local Similarity 77.8%; Pred. NO. 1.4e+04;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 ttaggatggtgcgcgc 20
|| ||||| |||
Db 18 TTTTGGATGGTTCGGTCA 1
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Search completed: October 2, 2001, 16:55:04
Job time: 17667 sec
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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run On: October 2, 2001, 21:50:15 ; Search time 17695.9 Seconds
(without alignments)
16.701 Million cell updates/sec

Title: US-09-757-100B-14

Perfect score: 20

Sequence: 1 ggtagggatggtgcgcgtca 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 14155048 seqs, 7388405095 residues

Total number of hits satisfying chosen parameters: 4519004

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 56: /cgn2_6/ptodata/1/pna/US6024_COMB.seq.*
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- 59: /cgn2_6/ptodata/1/pna/US6027_COMB.seq.*
- 60: /cgn2_6/ptodata/1/pna/US6028_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	20	100.0	20	17	US-09-377-310-14	Sequence 14, Appl
3	20	100.0	20	29	US-09-757-100B-14	Sequence 14, Appl
c	15.2	76.0	25	55	US-60-233-166-198784	Sequence 138784,
4	15	75.0	15	1	PCT-US00-18999-34	Sequence 34, Appl
5	15	75.0	15	17	US-09-377-310-34	Sequence 34, Appl
6	15	75.0	15	29	US-09-757-100B-34	Sequence 34, Appl
7	15	75.0	15	26	US-09-660-220-13935	Sequence 13935, A
8	14.2	71.0	25	55	US-60-232-638-39603	Sequence 39603, A
c	14.2	71.0	25	55	US-60-233-620-79723	Sequence 79723, A
9	14.2	71.0	25	55	US-60-234-017-255450	Sequence 255450,
10	14.2	71.0	34	14	US-09-004-729-58	Sequence 58, Appl
11	14.2	71.0	34	15	US-09-004-755-58	Sequence 58, Appl
12	14.2	71.0	34	15	US-09-171-741C-58	Sequence 58, Appl
13	14.2	71.0	34	15	US-09-171-741C-58	Sequence 1, Appl
14	14.2	71.0	34	15	US-09-171-741C-58	Sequence 1, Appl
c	13.8	69.0	24	3	US-07-896-094-1	Sequence 18, Appl
15	13.8	69.0	24	8	US-08-458-319-18	Sequence 118931,
16	13.8	69.0	25	26	US-09-660-220-118931	Sequence 118931,
17	13.8	69.0	25	26	US-60-234-017-472694	Sequence 472694,
18	13.8	69.0	25	55	US-60-234-049-141254	Sequence 141254,
c	13.8	69.0	25	55	US-60-234-049-141254	Sequence 62879, A
19	13.6	68.0	25	55	US-60-233-166-62879	Sequence 285311,
20	13.6	68.0	25	55	US-60-233-166-285311	Sequence 285312,
21	13.6	68.0	25	55	US-60-233-166-285311	Sequence 285313,
22	13.6	68.0	25	55	US-60-233-166-285315	Sequence 285315,
23	13.6	68.0	25	55	US-60-233-166-285315	Sequence 336370,
24	13.6	68.0	25	55	US-60-234-017-336370	Sequence 88046, A
25	13.6	68.0	25	55	US-60-234-049-88046	Sequence 120, App
26	13.6	68.0	18	1	PCT-US99-08268-120	Sequence 121, App
c	13.4	67.0	18	1	PCT-US99-08268-121	Sequence 11, Appl
27	13.4	67.0	18	1	PCT-US99-09085-11	Sequence 12, Appl
28	13.4	67.0	18	1	PCT-US99-09085-12	Sequence 120, App
29	13.4	67.0	18	16	US-09-295-463-120	Sequence 121, App
30	13.4	67.0	18	16	US-09-295-463-121	Sequence 113, App
31	13.4	67.0	18	17	US-09-387-341-113	Sequence 114, App
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38	13.2	66.0	25	55	US-60-233-166-94414	Sequence 590747,
39	13.2	66.0	25	55	US-60-234-017-590747	Sequence 98, Appl
40	13.2	66.0	33	3	US-07-958-143A-98	Sequence 98, Appl
41	13.2	66.0	33	3	US-07-958-143A-98	Sequence 147, App
42	13.2	66.0	40	25	US-09-645-706-147	Sequence 138406,
c	13.2	66.0	40	25	US-09-645-706-147	Sequence 138406,
43	12.8	64.0	25	55	US-60-234-049-138406	

ALIGNMENTS

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RESULT 1
PCT-US00-18999-14
; Sequence 14, Application PC/TUS0018999
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Monia, Brett P.
; APPLICANT: Gaarde, William A.
; APPLICANT: Nero, Pamela S.
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
; FILE REFERENCE: ISPH-0476
; CURRENT APPLICATION NUMBER: PCT/US00/18999
; CURRENT FILING DATE: 2000-07-13
; PRIOR APPLICATION NUMBER: 09/377,310
; PRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
PCT-US00-18999-14

Query Match          100.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ggttagggatggtgccgtca 20
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Db 1 ggttagggatggtgccgtca 20

RESULT 2
US-09-377-310-14
; Sequence 14, Application US/09377310A
; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P.
; APPLICANT: Gaarde, William A.
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
; FILE REFERENCE: ISPH-0389
; CURRENT APPLICATION NUMBER: US/09/377,310A
; CURRENT FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
US-09-377-310-14

Query Match          100.0%; Score 20; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ggttagggatggtgccgtca 20
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Db 1 ggttagggatggtgccgtca 20

RESULT 3
US-09-757-100B-14
; Sequence 14, Application US/09757100B
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; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P.
; APPLICANT: Gaarde, William A.
; APPLICANT: Nero, Pamela S.
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
; FILE REFERENCE: ISPH-0533
; CURRENT APPLICATION NUMBER: US/09/757,100B
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 09/377,310
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/US00/18999
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
US-09-757-100B-14

Query Match          100.0%; Score 20; DB 29; Length 20;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ggttagggatggtgccgtca 20
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Db 1 ggttagggatggtgccgtca 20

RESULT 4
US-60-233-166-198784/c
; Sequence 198784, Application US/60233166
; GENERAL INFORMATION:
; APPLICANT: Mitmann
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat
; TITLE OF INVENTION: Genome
; FILE REFERENCE: 3112
; CURRENT APPLICATION NUMBER: US/60/233,166
; CURRENT FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 420907
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 198784
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank AA998576
US-60-233-166-198784

Query Match          76.0%; Score 15.2; DB 55; Length 25;
Best Local Similarity 85.0%; Pred. No. 2.6e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ggttagggatggtgccgtca 20
   |||||
Db 25 GGTAGAGATGGATCCGTCA 6

RESULT 5
PCT-US00-18999-34
; Sequence 34, Application PC/TUS0018999
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Monia, Brett P.
; APPLICANT: Gaarde, William A.
; APPLICANT: Nero, Pamela S.
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
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; TITLE OF INVENTION: Expression
; FILE REFERENCE: ISPH-0476
; CURRENT APPLICATION NUMBER: PCT/US00/18999
; CURRENT FILING DATE: 2000-07-13
; PRIOR APPLICATION NUMBER: 09/377,310
; PRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 34
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
PCT-US00-18999-34

Query Match 75.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ttagggtggtgcgcg 17
|||||
Db 1 ttagggtggtgcgcg 15

RESULT 6
US-09-377-310-34
; Sequence 34, Application US/09377310A
; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P.
; APPLICANT: Gaarde, William A.
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
; FILE REFERENCE: ISPH-0389
; CURRENT APPLICATION NUMBER: US/09/377,310A
; CURRENT FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 34
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
US-09-377-310-34

Query Match 75.0%; Score 15; DB 17; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ttagggtggtgcgcg 17
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Db 1 ttagggtggtgcgcg 15

RESULT 7
US-09-757-100B-34
; Sequence 34, Application US/09757100B
; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P.
; APPLICANT: Gaarde, William A.
; APPLICANT: Nero, Pamela S.
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
; FILE REFERENCE: ISPH-0533
; CURRENT APPLICATION NUMBER: US/09/757,100B
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 09/377,310
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/US00/18999
; PRIOR FILING DATE: 2000-07-13

; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 34
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
US-09-757-100B-34

Query Match 75.0%; Score 15; DB 29; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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|||||
Db 1 ttagggtggtgcgcg 15

RESULT 8
US-09-660-220-13935
; Sequence 13935, Application US/09660220
; GENERAL INFORMATION:
; APPLICANT: Mittmann et al.
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of Human
; FILE REFERENCE: 3102.1
; CURRENT APPLICATION NUMBER: US/09/660,220
; CURRENT FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 60/164,973
; PRIOR FILING DATE: 1999-11-11
; NUMBER OF SEQ ID NOS: 140981
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13935
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank D83784
US-09-660-220-13935

Query Match 71.0%; Score 14.2; DB 26; Length 25;
Best Local Similarity 84.2%; Pred. No. 8.2e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ggttagggatggtgcgcgc 19
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Db 1 ggttagggatggtgcgcgc 19

RESULT 9
US-60-232-638-39603/c
; Sequence 39603, Application US/60232638
; GENERAL INFORMATION:
; APPLICANT: Mittmann
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of Yeast
; FILE REFERENCE: 3110
; CURRENT APPLICATION NUMBER: US/60/232,638
; CURRENT FILING DATE: 2000-09-14
; NUMBER OF SEQ ID NOS: 138410
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 39603
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: SGD YCL029C
US-60-232-638-39603

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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RESULT 12
US-09-004-729-58

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/004,755
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/749,699
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2618-25-C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (primer)
US-09-004-755-58

Query Match 71.0%; Score 14.2; DB 14; Length 34;
Best Local Similarity 84.2%; Pred. No. 8.3e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 gttaggatggtgccgtca 20
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Db 13 GTTAGCGATCGTCCGTCA 31

RESULT 14

US-09-171-741C-58
Sequence 58, Application US/09171741C
GENERAL INFORMATION:
APPLICANT: Grieve, Robert B.
APPLICANT: Rushlow, Keith E.
APPLICANT: Wu Hunter, Shirley
APPLICANT: Frank, Glenn R.
APPLICANT: Stiegler, Gary
APPLICANT: Gaines, Patrick J.
APPLICANT: Silver, Gary
TITLE OF INVENTION: FLEA PROTEASE PROTEINS, NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 2618-25-C4-PUS
CURRENT APPLICATION NUMBER: US/09/171,741C
CURRENT FILING DATE: 1999-04-23
PRIOR APPLICATION NUMBER: PCT/US97/06121
PRIOR FILING DATE: 1997-04-04
NUMBER OF SEQ ID NOS: 165
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 58
LENGTH: 34
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: primer
US-09-171-741C-58

Query Match 71.0%; Score 14.2; DB 15; Length 34;
Best Local Similarity 84.2%; Pred. No. 8.3e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 gttaggatggtgccgtca 20
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Db 13 GTTAGCGATCGTCCGTCA 31

RESULT 15
US-07-896-094-1/C
Sequence 1, Application US/07896094
GENERAL INFORMATION:
APPLICANT: Sheiness, Diana K.
APPLICANT: Adams, Trevor H.
APPLICANT: Stamm, Michael P.
APPLICANT: Cangelosi, Gerard A.
TITLE OF INVENTION: Methods and Pharmaceutical Kits Useful
TITLE OF INVENTION: for Detecting Microorganisms Associated with Vaginal
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/896,094
FILING DATE: 19920529
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen L.
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 11652-73-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (oligonucleotide)
US-07-896-094-1

Query Match 69.0%; Score 13.8; DB 3; Length 24;
Best Local Similarity 88.2%; Pred. No. 1.3e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 18 TTTGGGATGGAGCCGTC 2

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Job time: 24528 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: October 2, 2001, 21:50:14 ; Search time 17695.9 Seconds
(without alignments)
16.701 Million cell updates/sec

Title: US-09-757-100B-12

Perfect score: 20

Sequence: 1 cctgacatcagtagcatctc 20

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Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters: 4519004

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Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

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SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
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2	20	100.0	20	17	US-09-377-310-12	Sequence 12, Appl
3	20	100.0	20	29	US-09-757-100B-12	Sequence 16, Appl
c 4	16.4	82.0	20	1	PCT-US00-07678-16	Sequence 16, Appl
5	16.4	82.0	20	20	US-09-535-008-16	Sequence 16, Appl
6	15.8	79.0	25	55	US-60-233-166-196919	Sequence 196919,
c 7	15.8	79.0	25	55	US-60-233-166-296426	Sequence 296426,
8	15	75.0	15	1	PCT-US00-18999-32	Sequence 32, Appl
9	15	75.0	15	17	US-09-377-310-32	Sequence 32, Appl
10	15	75.0	15	29	US-09-757-100B-32	Sequence 32, Appl
c 11	14.8	74.0	20	30	US-09-794-422-41	Sequence 41, Appl
12	14.2	71.0	25	55	US-60-233-166-198167	Sequence 198167,
13	14.2	71.0	25	55	US-60-233-166-198168	Sequence 198168,
14	14.2	71.0	25	55	US-60-233-166-303481	Sequence 303481,
c 15	13.8	69.0	17	8	US-08-435-632-1431	Sequence 1431, Ap
c 16	13.8	69.0	17	11	US-08-777-920-1431	Sequence 1431, Ap
c 17	13.8	69.0	21	25	US-09-657-472-257	Sequence 257, App
c 18	13.8	69.0	25	55	US-60-232-638-119646	Sequence 119646,
19	13.8	69.0	25	55	US-60-233-166-6055	Sequence 6055, Ap
20	13.8	69.0	25	55	US-60-233-166-226952	Sequence 226952,
c 21	13.6	68.0	25	55	US-60-233-166-290790	Sequence 290790,
c 22	13.6	68.0	25	55	US-09-660-220-81834	Sequence 81834, A
c 23	13.6	68.0	25	55	US-60-234-017-13449	Sequence 13449, A
24	13.6	68.0	25	55	US-60-234-017-361774	Sequence 361774,
c 25	13.6	68.0	25	55	US-60-234-049-104369	Sequence 104369,
c 26	13.6	68.0	39	1	PCT-US99-29963-38	Sequence 38, Appl
c 27	13.6	68.0	40	1	PCT-US99-29963-37	Sequence 37, Appl
c 28	13.6	68.0	42	3	US-07-904-068A-64	Sequence 64, Appl
c 29	13.6	68.0	42	5	US-08-161-739-64	Sequence 64, Appl
c 30	13.6	68.0	42	5	US-08-165-699-64	Sequence 64, Appl
c 31	13.6	68.0	42	11	US-08-728-463-36	Sequence 36, Appl
c 32	13.6	68.0	42	11	US-08-728-463-73	Sequence 73, Appl
c 33	13.6	68.0	42	11	US-08-728-463B-36	Sequence 36, Appl
c 34	13.6	68.0	42	11	US-08-728-463B-73	Sequence 73, Appl
c 35	13.6	68.0	42	11	US-08-758-417-36	Sequence 36, Appl
c 36	13.6	68.0	42	11	US-08-758-417-73	Sequence 73, Appl
c 37	13.6	68.0	42	11	US-08-758-417A-36	Sequence 36, Appl
c 38	13.6	68.0	42	11	US-08-758-417A-73	Sequence 73, Appl
c 39	13.4	67.0	25	26	US-09-660-220-138856	Sequence 138856,
c 40	13.4	67.0	25	26	US-09-660-220-138858	Sequence 138858,
c 41	13.4	67.0	25	26	US-09-660-220-138859	Sequence 138859,
c 42	13.4	67.0	25	55	US-60-232-638-14816	Sequence 14816, A
c 43	13.4	67.0	25	55	US-60-233-166-296504	Sequence 296504,
c 44	13.2	66.0	21	17	US-09-357-273A-11	Sequence 11, Appl
c 45	13.2	66.0	25	55	US-60-233-166-147576	Sequence 147576,

ALIGNMENTS

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RESULT 1
PCT-US00-18999-12
; Sequence 12, Application PC/TUS0018999
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Monia, Brett P.
; APPLICANT: Gaarde, William A.
; APPLICANT: Nero, Pamela S.
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
; FILE REFERENCE: ISPH-0476
; CURRENT APPLICATION NUMBER: PCT/US00/18999
; CURRENT FILING DATE: 2000-07-13
; PRIOR APPLICATION NUMBER: 09/377,310
; PRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
PCT-US00-18999-12

Query Match 100.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cctgacatcagtagcatctc 20
Db 1 cctgacatcagtagcatctc 20
|||||

RESULT 2
US-09-377-310-12
; Sequence 12, Application US/09377310A
; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P.
; APPLICANT: Gaarde, William A.
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
; FILE REFERENCE: ISPH-0389
; CURRENT APPLICATION NUMBER: US/09/377,310A
; CURRENT FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
US-09-377-310-12

Query Match 100.0%; Score 20; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cctgacatcagtagcatctc 20
Db 1 cctgacatcagtagcatctc 20
|||||

RESULT 3
US-09-757-100B-12
; Sequence 12, Application US/09757100B
```

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; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P.
; APPLICANT: Gaarde, William A.
; APPLICANT: Nero, Pamela S.
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
; FILE REFERENCE: ISPH-0533
; CURRENT APPLICATION NUMBER: US/09/757,100B
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 09/377,310
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/US00/18999
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
US-09-757-100B-12

Query Match 100.0%; Score 20; DB 29; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cctgacatcagtagcatctc 20
Db 1 cctgacatcagtagcatctc 20
|||||

RESULT 4
PCT-US00-07678-16/c
; Sequence 16, Application PC/TUS0007678
; GENERAL INFORMATION:
; APPLICANT: Wong, Alexander K.C.
; APPLICANT: Tavtigian, Sean V.
; APPLICANT: Teng, David H.-F.
; APPLICANT: Myriad Genetics, Inc.
; TITLE OF INVENTION: BRG1 IS A TUMOR SUPPRESSOR THAT IS MUTATED IN PROSTATE
; FILE REFERENCE: 2318-259-PCT
; CURRENT APPLICATION NUMBER: PCT/US00/07678
; CURRENT FILING DATE: 2000-03-23
; EARLIER APPLICATION NUMBER: U.S. 60/125,806
; EARLIER FILING DATE: 1999-03-23
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US00-07678-16

Query Match 82.0%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 6.1e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ctgacatcagtagcatctc 19
Db 20 CTGGCATCAGTAGCATCT 3
|||||

RESULT 5
US-09-535-008-16/c
; Sequence 16, Application US/09535008
; GENERAL INFORMATION:
; APPLICANT: Wong, Alexander K.C.
; APPLICANT: Tavtigian, Sean V.
; APPLICANT: Teng, David H.-F.
```

; TITLE OF INVENTION: BRG1 IS A TUMOR SUPPRESSOR THAT IS MUTATED IN PROSTATE
; FILE OF INVENTION: AND OTHER CANCER TYPES
; FILE REFERENCE: 2318-259
; CURRENT APPLICATION NUMBER: US/09/535,008
; CURRENT FILING DATE: 2000-03-23
; EARLIER APPLICATION NUMBER: U.S. 60/125,806
; EARLIER FILING DATE: 1999-03-23
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-535-008-16

Query Match 82.0%; Score 16.4; DB 20; Length 20;
Best Local Similarity 94.4%; Pred. No. 6.1e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ctgacatcagtagcatct 19
||| ||||| ||||| |||||
Db 20 CTGCATCAGTAGCATCT 3

RESULT 6
US-60-233-166-196919/c
; Sequence 196919, Application US/60233166
; GENERAL INFORMATION:
; APPLICANT: Mittmann
; TITLE OF INVENTION: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat
; FILE REFERENCE: 3112
; CURRENT APPLICATION NUMBER: US/60/233,166
; CURRENT FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 420907
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 196919
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank AA998576
US-60-233-166-196919

Query Match 79.0%; Score 15.8; DB 55; Length 25;
Best Local Similarity 89.5%; Pred. No. 1.2e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 cctgacatcagtagcatct 19
||||| ||||| ||||| |||||
Db 19 CCTGACACCAAGCATCT 1

RESULT 7
US-60-233-166-296426/c
; Sequence 296426, Application US/60233166
; GENERAL INFORMATION:
; APPLICANT: Mittmann
; TITLE OF INVENTION: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat
; FILE REFERENCE: 3112
; CURRENT APPLICATION NUMBER: US/60/233,166
; CURRENT FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 420907
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 296426
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus

; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank AI639536
US-60-233-166-296426

Query Match 79.0%; Score 15.8; DB 55; Length 25;
Best Local Similarity 89.5%; Pred. No. 1.2e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ctgacatcagtagcatctc 20
||||| ||||| ||||| |||||
Db 22 CTGCATAAGTAGCACCTC 4

RESULT 8
PCT-US00-18999-32
; Sequence 32, Application PC/TUS0018999
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Monia, Brett P.
; APPLICANT: Gaarde, William A.
; APPLICANT: Nero, Pamela S.
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
; TITLE OF INVENTION: Expression
; FILE REFERENCE: ISPH-0476
; CURRENT APPLICATION NUMBER: PCT/US00/18999
; CURRENT FILING DATE: 2000-07-13
; PRIOR APPLICATION NUMBER: 09/377,310
; PRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 32
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
PCT-US00-18999-32

Query Match 75.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 tgacatcagtagcat 17
||||| ||||| ||||| |||||
Db 1 tgacatcagtagcat 15

RESULT 9
US-09-377-310-32
; Sequence 32, Application US/09377310A
; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P.
; APPLICANT: Gaarde, William A.
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
; TITLE OF INVENTION: Expression
; FILE REFERENCE: ISPH-0389
; CURRENT APPLICATION NUMBER: US/09/377,310A
; CURRENT FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 32
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
US-09-377-310-32

Query Match 75.0%; Score 15; DB 17; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 tgacatcagtagcat 17
| | | | | | | | | | | | | | | | | | | | |
Db 1 tgacatcagtagcat 15

RESULT 10
US-09-757-100B-32
; Sequence 32, Application US/09757100B
; GENERAL INFORMATION:
; APPLICANT: Monla, Brett P.
; APPLICANT: Gaarde, William A.
; APPLICANT: Nero, Pamela S.
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
; FILE REFERENCE: ISPH-0533
; CURRENT APPLICATION NUMBER: US/09/757,100B
; CURRENT FILING DATE: 2001-03-15
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/US00/18999
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 32
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
US-09-757-100B-32

Query Match 75.0%; Score 15; DB 29; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 tgacatcagtagcat 17
| | | | | | | | | | | | | | | | | | | | |
Db 1 tgacatcagtagcat 15

RESULT 11
US-09-794-422-41/c
; Sequence 41, Application US/09794422
; GENERAL INFORMATION:
; APPLICANT: Brown, Thomas A.
; APPLICANT: De Wet, Jeffrey R.
; APPLICANT: Gowen, Lori C.
; APPLICANT: Hames, Lynn M.
; TITLE OF INVENTION: Mammalian Osteoregulins
; FILE REFERENCE: PC10445
; CURRENT APPLICATION NUMBER: US/09/794,422
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 60/185,617
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: 60/234,500
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 41
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-794-422-41

Query Match 74.0%; Score 14.8; DB 30; Length 20;
Best Local Similarity 88.9%; Pred. No. 3.8e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ctgacatcagtagcatct 19

Db 18 CTGACATCAACAGCATCT 1
| | | | | | | | | | | | | | | | | | | | |

RESULT 12
US-60-233-166-198167
; Sequence 198167, Application US/60233166
; GENERAL INFORMATION:
; APPLICANT: Affymetrix, Inc.
; APPLICANT: Mittmann
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat
; FILE REFERENCE: 3112
; CURRENT APPLICATION NUMBER: US/60/233,166
; CURRENT FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 420907
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 198167
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank AA998576
US-60-233-166-198167

Query Match 71.0%; Score 14.2; DB 55; Length 25;
Best Local Similarity 84.2%; Pred. No. 7.9e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 ctgacatcagtagcatctc 20
| | | | | | | | | | | | | | | | | | | | |
Db 2 cggacaccagtagcatcac 20

RESULT 13
US-60-233-166-198168
; Sequence 198168, Application US/60233166
; GENERAL INFORMATION:
; APPLICANT: Affymetrix, Inc.
; APPLICANT: Mittmann
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat
; FILE REFERENCE: 3112
; CURRENT APPLICATION NUMBER: US/60/233,166
; CURRENT FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 420907
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 198168
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank AA998576
US-60-233-166-198168

Query Match 71.0%; Score 14.2; DB 55; Length 25;
Best Local Similarity 84.2%; Pred. No. 7.9e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 ctgacatcagtagcatctc 20
| | | | | | | | | | | | | | | | | | | | |
Db 5 cggacaccagtagcatcac 23

RESULT 14
US-60-233-166-303481
; Sequence 303481, Application US/60233166
; GENERAL INFORMATION:
; APPLICANT: Mittmann
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat

;; TITLE OF INVENTION: Genome
;; RILE REFERENCE: 3112
;; CURRENT APPLICATION NUMBER: US/60/233,166
;; CURRENT FILING DATE: 2000-10-24
;; NUMBER OF SEQ ID NOS: 420907
;; SOFTWARE: FastSEQ for Windows Version 4.0
;; SEQ ID NO 303481
;; LENGTH: 25
;; TYPE: DNA
;; ORGANISM: Rattus norvegicus
;; PUBLICATION INFORMATION:
;; DATABASE ACCESSION NUMBER: GenBank D10757
US-60-233-166-303481

Query Match 71.0%; Score 14.2; DB 55; Length 25;
Best Local Similarity 84.2%; Pred. No. 7.9e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 cctgacatcagtagcatct 19
||||| |||||
Db 3 cctgaagtgcagtagcatct 21

RESULT 15
US-08-435-632-1431/c
;; Sequence 1431, Application US/08435632
;; GENERAL INFORMATION:
;; APPLICANT: Stinchcomb, Dan T.
;; APPLICANT: Draper, Kenneth
;; APPLICANT: McSwiggen, James
;; APPLICANT: Jarvis, Thale
;; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
;; TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
;; TITLE OF INVENTION: CANCER USING RIBOZYMES
;; NUMBER OF SEQUENCES: 2627
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Lyon & Lyon
;; STREET: 633 West Fifth Street
;; CITY: Suite 4700
;; CITY: Los Angeles
;; STATE: California
;; COUNTRY: U.S.A.
;; ZIP: 90071

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/435,632
FILING DATE: 05-MAY-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/373,124
FILING DATE: January 13, 1995
APPLICATION NUMBER: 08/245,466
FILING DATE: May 18, 1994
APPLICATION NUMBER: 08/192,943
FILING DATE: February 7, 1994
APPLICATION NUMBER: 07/987,132
FILING DATE: December 7, 1992
APPLICATION NUMBER: 07/936,422
FILING DATE: August 26, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 209/035
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510

;; INFORMATION FOR SEQ ID NO: 1431:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 17 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
US-08-435-632-1431

Query Match 69.0%; Score 13.8; DB 8; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.2e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 4 gacatcagtagcatctc 20
||||| |||||
Db 17 GACATCAGGAGCACTC 1

Search completed: October 2, 2001, 21:50:15
Job time: 24528 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: October 2, 2001, 12:00:36 ; Search time 417.38 Seconds
(without alignments)
9.071 Million cell updates/sec

Title: US-09-757-100B-3

Perfect score: 20

Sequence: 1 ccgcgggctcacagtgtcg 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 324599 seqs, 9465562 residues

Total number of hits satisfying chosen parameters: 460742

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_NA.*

- 1: /cgn2_6/ptodata/1/ina/5A_COMB.seq.*
- 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*
- 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*
- 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*
- 5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq.*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	3	US-09-377-310-3
2	15	75.0	15	3	US-09-377-310-23
3	13.8	69.0	31	3	US-09-282-996-18
4	13.2	66.0	33	1	US-08-361-337-41
5	12.2	61.0	18	3	US-09-344-579-40
6	12.2	61.0	31	2	US-08-732-612-6
7	12.2	61.0	39	2	US-08-732-612-11
8	12.2	61.0	40	3	US-09-135-639-8
9	12.2	61.0	40	3	US-09-135-639-10
10	12.2	61.0	50	4	US-09-315-886C-5
11	12	60.0	41	3	US-08-751-359-9
12	11.8	59.0	16	1	US-08-640-378-13
13	11.8	59.0	22	1	US-08-242-403A-38
14	11.8	59.0	22	1	US-08-774-128-38
15	11.8	59.0	22	5	PCT-US95-05602-38
16	11.8	59.0	22	5	PCT-US95-05816-38
17	11.8	59.0	29	1	US-08-640-378-3
18	11.8	59.0	30	1	US-08-640-378-4
19	11.8	59.0	30	1	US-08-640-378-5
20	11.8	59.0	35	1	US-08-289-953-1
21	11.8	59.0	35	5	PCT-US95-09195-1
22	11.8	59.0	36	1	US-07-744-282C-19
23	11.8	59.0	36	5	PCT-US92-06821A-19
24	11.8	59.0	44	1	US-08-242-403A-34
25	11.8	59.0	44	1	US-08-774-128-34
26	11.8	59.0	44	5	PCT-US95-05602-34
27	11.8	59.0	44	5	PCT-US95-05816-34

28	11.6	58.0	24	1	US-08-139-540-8	Sequence 8, Appli
29	11.6	58.0	24	1	US-08-634-826-8	Sequence 8, Appli
30	11.6	58.0	24	3	US-09-115-175-8	Sequence 8, Appli
c 31	11.6	58.0	25	1	US-08-096-947-6	Sequence 6, Appli
32	11.6	58.0	25	1	US-08-096-947-7	Sequence 7, Appli
c 33	11.6	58.0	25	1	US-08-096-947-9	Sequence 9, Appli
c 34	11.6	58.0	25	1	US-07-919-140B-6	Sequence 6, Appli
c 35	11.6	58.0	25	1	US-07-919-140B-7	Sequence 7, Appli
c 36	11.6	58.0	25	1	US-07-919-140B-9	Sequence 9, Appli
37	11.6	58.0	25	1	US-08-924-763-7	Sequence 7, Appli
38	11.6	58.0	25	3	US-08-617-256-12	Sequence 12, Appli
39	11.6	58.0	25	4	US-09-287-141-12	Sequence 12, Appli
40	11.6	58.0	25	4	US-09-431-613-12	Sequence 12, Appli
41	11.6	58.0	25	4	US-09-504-245-12	Sequence 12, Appli
42	11.6	58.0	25	4	US-09-287-682-12	Sequence 12, Appli
43	11.6	58.0	25	4	US-09-358-972-246	Sequence 246, App
44	11.6	58.0	25	4	US-09-397-766-12	Sequence 12, Appli
c 45	11.6	58.0	25	5	PCT-US93-06939-9	Sequence 9, Appli

ALIGNMENTS

RESULT 1
US-09-377-310-3
; Sequence 3, Application US/09377310B
; Patent No. 6133031
; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P.
; APPLICANT: Gaarde, William A.
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
; FILE REFERENCE: ISPH-0389
; CURRENT APPLICATION NUMBER: US/09/377,310B
; CURRENT FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
US-09-377-310-3

Query Match 100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ccgcgggctcacagtgtcg 20
Db 1 ccgcgggctcacagtgtcg 20
|||||

RESULT 2
US-09-377-310-23
; Sequence 23, Application US/09377310B
; Patent No. 6133031
; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P.
; APPLICANT: Gaarde, William A.
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
; FILE REFERENCE: ISPH-0389
; CURRENT APPLICATION NUMBER: US/09/377,310B
; CURRENT FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence

```
;
; FEATURE:
; OTHER INFORMATION: antisense sequence
US-09-377-310-23

Query Match      75.0%; Score 15; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 gcggggtcacagtgg 17
    |||||
DB 1 gcggggtcacagtgg 15

RESULT 3
US-09-282-996-18/c
; Sequence 18, Application US/09282996
; Patent No. 6143502
; GENERAL INFORMATION:
; APPLICANT: Grentzmann, Guido
; APPLICANT: Gesteland, Raymond F.
; APPLICANT: Atkins, John F.
; TITLE OF INVENTION: Dual-Luciferase Reporter System
; FILE REFERENCE: T5864.NP
; CURRENT APPLICATION NUMBER: US/09/282.996
; CURRENT FILING DATE: 1999-03-31
; EARLIER APPLICATION NUMBER:
; EARLIER FILING DATE:
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: WordPerfect 8.0
; SEQ ID NO 18
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer fsA22
US-09-282-996-18

Query Match      69.0%; Score 13.8; DB 3; Length 31;
Best Local Similarity 88.2%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ccgcgggtcacagtgg 17
    |||||
DB 25 CACGGGATCACAGTGG 9

RESULT 4
US-08-361-337-41
; Sequence 41, Application US/08361337
; Patent No. 5728519
; GENERAL INFORMATION:
; APPLICANT: Levenbook, Inessa S.
; APPLICANT: Chumakov, Konstantin M.
; APPLICANT: No. 5728519wood, Laurie P.
; APPLICANT: Roninson, Igor
; TITLE OF INVENTION: ASSAY FOR VIRULENT REVERTANTS OF
; TITLE OF INVENTION: ATTENUATED LIVE VACCINES
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NEEDLE & ROSENBERG, P.C.
; STREET: 127 Peachtree Street, N.E.
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/361.337
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Perryman, David G.
; REGISTRATION NUMBER: 33,438
; REFERENCE/DOCKET NUMBER: 1414.634
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 688-0770
; TELEFAX: (404) 688-9880
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid
US-08-361-337-41

Query Match      66.0%; Score 13.2; DB 1; Length 33;
Best Local Similarity 83.3%; Pred. No. 3.8e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ccgcgggtcacagtgg 18
    |||||
DB 9 CCGGGGTTCAAAGTAGT 26

RESULT 5
US-09-344-579-40
; Sequence 40, Application US/09344579
; Patent No. 6054316
; GENERAL INFORMATION:
; APPLICANT: Brenda F. Baker
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF ETS-2 EXPRESSION
; FILE REFERENCE: RTS-0063
; CURRENT APPLICATION NUMBER: US/09/344.579
; CURRENT FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 40
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-344-579-40

Query Match      61.0%; Score 12.2; DB 3; Length 18;
Best Local Similarity 82.4%; Pred. No. 1.1e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 gcggggtcacagtggtc 19
    |||||
DB 2 gccgggtcagggtggtc 18

RESULT 6
US-08-732-612-6
; Sequence 6, Application US/08732612
; Patent No. 5922583
; GENERAL INFORMATION:
; APPLICANT: MORSEY, MOHAMAD A.
; TITLE OF INVENTION: METHODS FOR PRODUCTION OF RECOMBINANT
; TITLE OF INVENTION: PLASMIDS
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 PENNSYLVANIA AVE., NW
; CITY: WASHINGTON
; STATE: DC
```

COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/732,612
FILING DATE: 16-OCT-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 29311-20006.21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
TELEX: 90-4030 MRSNFOERSWSH
SEQUENCE CHARACTERISTICS:
LENGTH: 31 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: prim.transcript
LOCATION: 1..31
OTHER INFORMATION: /note= "downstream primer
INFORMATION FOR SEQ ID NO: 6:
US-08-732-612-6

Query Match 61.0%; Score 12.2; DB 2; Length 31;
Best Local Similarity 82.4%; Pred. No. 1.2e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ccgcggggtcacagtgg 17
||| ||||| |||||
Db 10 CAGCAGGCTGACAGTGG 26

RESULT 7
US-08-732-612-11
Sequence 11, Application US/08732612
Patent No. 5922583
GENERAL INFORMATION:
APPLICANT: MORSEY, MOHAMAD A.
TITLE OF INVENTION: METHODS FOR PRODUCTION OF RECOMBINANT
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 PENNSYLVANIA AVE., NW
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/732,612
FILING DATE: 16-OCT-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 29311-20006.21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500

TELEFAX: (202) 887-0763
TELEX: 90-4030 MRSNFOERSWSH
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: prim.transcript
LOCATION: 1..39
OTHER INFORMATION: /note= "downstream primer
OTHER INFORMATION: designated murf4"
US-08-732-612-11

Query Match 61.0%; Score 12.2; DB 2; Length 39;
Best Local Similarity 82.4%; Pred. No. 1.2e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ccgcggggtcacagtgg 17
||| ||||| |||||
Db 18 CAGCAGGCTGACAGTGG 34

RESULT 8
US-09-135-639-8
Sequence 8, Application US/09135639
Patent No. 6004793
GENERAL INFORMATION:
APPLICANT: LUNNEN, KEITH D.
APPLICANT: WILSON, GEOFFREY G.
APPLICANT: XU, SHUANG-YONG
TITLE OF INVENTION: Method For Cloning And Producing The Avai Restriction
TITLE OF INVENTION: Endonuclease In E. coli And Purification Of The
TITLE OF INVENTION: Recombinant Avai Restriction Endonuclease
FILE REFERENCE: Avai
CURRENT APPLICATION NUMBER: US/09/135,639
CURRENT FILING DATE: 1998-08-18
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 8
LENGTH: 40
TYPE: DNA
ORGANISM: Anabaena variabilis
US-09-135-639-8

Query Match 61.0%; Score 12.2; DB 3; Length 40;
Best Local Similarity 82.4%; Pred. No. 1.2e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ccgcggggtcacagtgg 17
||| ||||| |||||
Db 8 ccccggggtcaagtgg 24

RESULT 9
US-09-135-639-10
Sequence 10, Application US/09135639
Patent No. 6004793
GENERAL INFORMATION:
APPLICANT: LUNNEN, KEITH D.
APPLICANT: DALTON MICHAEL A.,
APPLICANT: WILSON, GEOFFREY G.
APPLICANT: XU, SHUANG-YONG
TITLE OF INVENTION: Method For Cloning And Producing The Avai Restriction
TITLE OF INVENTION: Endonuclease In E. coli And Purification Of The
TITLE OF INVENTION: Recombinant Avai Restriction Endonuclease
FILE REFERENCE: Avai
CURRENT APPLICATION NUMBER: US/09/135,639
CURRENT FILING DATE: 1998-08-18

; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 40
; TYPE: DNA
; ORGANISM: Anabaena variabilis
US-09-135-639-10

Query Match 61.0%; Score 12.2; DB 3; Length 40;
Best Local Similarity 82.4%; Pred. No. 1.2e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ccgcgggtcacagtgg 17
||| ||||| |||
Db 8 ccccggtctcaagtgg 24

RESULT 10
US-09-315-886C-5
; Sequence 5, Application US/09315886C
; Patent No. 6225063
; GENERAL INFORMATION:
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Yarus, Michael
; TITLE OF INVENTION: RNA Channels in Biological Membranes
; FILE REFERENCE: UTC-03444
; CURRENT APPLICATION NUMBER: US/09/315,886C
; CURRENT FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 60/086,492
; PRIOR FILING DATE: 1998-05-22
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 50
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
US-09-315-886C-5

Query Match 61.0%; Score 12.2; DB 4; Length 50;
Best Local Similarity 64.7%; Pred. No. 1.2e+03;
Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 3 gcggggtcacagtgtc 19
||| :|||:|:|
Db 23 gggggguucacagugauc 39

RESULT 11
US-08-751-359-9/C
; Sequence 9, Application US/08751359
; Patent No. 6143559
; GENERAL INFORMATION:
; APPLICANT: Michael, Nancy M
; APPLICANT: Accavitti, Marianne
; APPLICANT: Thompson, Craig B
; TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF CHICKEN
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P. O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/751,359
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 510
; ATTORNEY/AGENT INFORMATION:
; NAME: Highlander, Steven L
; REGISTRATION NUMBER: 37,642
; REFERENCE/DOCKET NUMBER: ARSB:504
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 41 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-751-359-9

Query Match 60.0%; Score 12; DB 3; Length 41;
Best Local Similarity 75.0%; Pred. No. 1.5e+03;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 ccgcgggtcacagtgtcg 20
||| ||||| |||
Db 24 CCCCGTGCACAGTCATCG 5

RESULT 12
US-08-640-378-13/c
; Sequence 13, Application US/08640378
; Patent No. 5811269
; GENERAL INFORMATION:
; APPLICANT: Nadeau, James G.
; APPLICANT: Dean, Cheryl H.
; APPLICANT: Schram, James L.
; APPLICANT: Howard, Deborah R.
; APPLICANT: Dey, Margaret S.
; APPLICANT: Wright, David J.
; TITLE OF INVENTION: DETECTION OF MYCOBACTERIA BY MULTIPLEX
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Richard J. Rodrick, Becton Dickinson and
; ADDRESSEE: Company
; STREET: 1 Becton Drive
; CITY: Franklin Lakes
; STATE: NJ
; COUNTRY: US
; ZIP: 07417
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/640,378
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Fugit, Donna R.
; REGISTRATION NUMBER: 32,135
; REFERENCE/DOCKET NUMBER: P-3625
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-640-378-13

Query Match 59.0%; Score 11.8; DB 1; Length 16;
Best Local Similarity 86.7%; Pred. No. 1.8e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ccgcgggctcacagt 15
||||| |||||

Db 15 CCGCATGCTCACAGT 1

RESULT 13

US-08-242-403A-38
; Sequence 38, Application US/08242403A
; Patent No. 5631130
; GENERAL INFORMATION:
; APPLICANT: Leckie, G. W.
; APPLICANT: Davis, A. H.
; APPLICANT: Sample-Facey, I. E.
; APPLICANT: Manlove, M. T.
; APPLICANT: Solomon, N. A.
; TITLE OF INVENTION: Materials and Methods for the Detection of
; MYCOBACTERIA TUBERCULOSIS
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: One Abbott Park Road
; CITY: Abbott Park
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PCDOS/MSDOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/242,403A
; FILING DATE: May 13, 1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Thomas D. Brainard
; REGISTRATION NUMBER: 32,459
; REFERENCE/DOCKET NUMBER: 5370.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708/937-4884
; TELEFAX: 708/938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Synthetic DNA

US-08-242-403A-38

Query Match 59.0%; Score 11.8; DB 1; Length 22;
Best Local Similarity 86.7%; Pred. No. 1.8e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ccgcgggctcacagt 15
||||| |||||

Db 7 CCGCAGCTCACAGT 21

RESULT 14

US-08-774-128-38
; Sequence 38, Application US/08774128
; Patent No. 5786149
; GENERAL INFORMATION:
; APPLICANT: Leckie, G. W.
; APPLICANT: Davis, A. H.

; APPLICANT: Sample-Facey, I. E.
; APPLICANT: Manlove, M. T.
; APPLICANT: Solomon, N. A.
; TITLE OF INVENTION: Materials and Methods for the Detection of
; MYCOBACTERIA TUBERCULOSIS
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: One Abbott Park Road
; CITY: Abbott Park
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PCDOS/MSDOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/774,128
; FILING DATE: 23-DEC-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/242,403
; FILING DATE: May 13, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Thomas D. Brainard
; REGISTRATION NUMBER: 32,459
; REFERENCE/DOCKET NUMBER: 5370.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708/937-4884
; TELEFAX: 708/938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Synthetic DNA

US-08-774-128-38

Query Match 59.0%; Score 11.8; DB 1; Length 22;
Best Local Similarity 86.7%; Pred. No. 1.8e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ccgcgggctcacagt 15
||||| |||||

Db 7 CCGCAGCTCACAGT 21

RESULT 15

PCT-US95-05602-38
; Sequence 38, Application PC/TUS9505602
; GENERAL INFORMATION:
; APPLICANT: Leckie, G. W.
; APPLICANT: Davis, A. H.
; APPLICANT: Sample-Facey, I. E.
; APPLICANT: Manlove, M. T.
; APPLICANT: Solomon, N. A.
; TITLE OF INVENTION: Materials and Methods for the Detection of
; MYCOBACTERIA TUBERCULOSIS
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: One Abbott Park Road
; CITY: Abbott Park
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC_DOS/MS_DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05602
FILING DATE: May 13, 1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Thomas D. Brainard
REGISTRATION NUMBER: 32,459
REFERENCE/DOCKET NUMBER: 5370.PC.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708/937-4884
TELEFAX: 708/938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Synthetic DNA
PCT-US95-05602-38

Query Match 59.0%; Score 11.8; DB 5; Length 22;
Best Local Similarity 86.7%; Pred. NO. 1.8e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ccgcggggtcacagt 15
||| |||||
Db 7 CCGCACGCTCACAGT 21

Search completed: October 2, 2001, 16:03:44
Job time: 14588 sec

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OM nucleic - nucleic search, using sw model

Run on: October 2, 2001, 21:50:13 ; Search time 17695.9 Seconds
(without alignments)
16.701 Million cell updates/sec

Title: US-09-757-100B-11

Perfect score: 20

Sequence: 1 agtaccaggtagctttag 20

Scoring table: IDENTITY_NUC

Gap 10.0 , Gapext 1.0

Searched: 1415048 seqs, 7388405095 residues

Total number of hits satisfying chosen parameters: 4519004

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3: /cgn2_6/ptodata/1/pna/US07_COMB.seq.*

4: /cgn2_6/ptodata/1/pna/US08_COMB.seq.*

5: /cgn2_6/ptodata/1/pna/US081_COMB.seq.*

6: /cgn2_6/ptodata/1/pna/US082_COMB.seq.*

7: /cgn2_6/ptodata/1/pna/US083_COMB.seq.*

8: /cgn2_6/ptodata/1/pna/US084_COMB.seq.*

9: /cgn2_6/ptodata/1/pna/US085_COMB.seq.*

10: /cgn2_6/ptodata/1/pna/US086_COMB.seq.*

11: /cgn2_6/ptodata/1/pna/US087_COMB.seq.*

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23: /cgn2_6/ptodata/1/pna/US096A_COMB.seq.*

24: /cgn2_6/ptodata/1/pna/US096B_COMB.seq.*

25: /cgn2_6/ptodata/1/pna/US096C_COMB.seq.*

26: /cgn2_6/ptodata/1/pna/US096D_COMB.seq.*

27: /cgn2_6/ptodata/1/pna/US096E_COMB.seq.*

28: /cgn2_6/ptodata/1/pna/US097A_COMB.seq.*

29: /cgn2_6/ptodata/1/pna/US097B_COMB.seq.*

30: /cgn2_6/ptodata/1/pna/US097C_COMB.seq.*

31: /cgn2_6/ptodata/1/pna/US098_COMB.seq.*

32: /cgn2_6/ptodata/1/pna/US099_COMB.seq.*

33: /cgn2_6/ptodata/1/pna/US099A_COMB.seq.*

34: /cgn2_6/ptodata/1/pna/US099B_COMB.seq.*

35: /cgn2_6/ptodata/1/pna/US099C_COMB.seq.*

36: /cgn2_6/ptodata/1/pna/US099D_COMB.seq.*

37: /cgn2_6/ptodata/1/pna/US099E_COMB.seq.*

38: /cgn2_6/ptodata/1/pna/US099F_COMB.seq.*

39: /cgn2_6/ptodata/1/pna/US099G_COMB.seq.*

40: /cgn2_6/ptodata/1/pna/US099H_COMB.seq.*

41: /cgn2_6/ptodata/1/pna/US099I_COMB.seq.*

42: /cgn2_6/ptodata/1/pna/US099J_COMB.seq.*

43: /cgn2_6/ptodata/1/pna/US099K_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	20	100.0	20	1	PCT-US00-18999-11	Sequence 11, Appl
2	20	100.0	20	17	US-09-377-310-11	Sequence 11, Appl
3	20	100.0	20	29	US-09-757-100B-11	Sequence 11, Appl
4	15.8	79.0	25	55	US-60-233-166-320910	Sequence 320910,
5	15.8	79.0	25	55	US-60-233-166-320910	Sequence 320910,
6	15.2	76.0	25	55	US-60-233-166-329526	Sequence 329526,
7	15.2	76.0	25	55	US-60-233-166-329643	Sequence 329643,
8	15.2	76.0	25	55	US-60-233-166-329644	Sequence 329644,
9	15	75.0	15	1	PCT-US00-18999-31	Sequence 31, Appl
10	15	75.0	15	17	US-09-377-310-31	Sequence 31, Appl
11	15	75.0	15	29	US-09-757-100B-31	Sequence 31, Appl
12	14.8	74.0	25	55	US-60-234-017-22548	Sequence 22548, A
13	14.4	72.0	25	55	US-60-233-620-18028	Sequence 18028, A
14	14.2	71.0	25	55	US-60-234-017-142091	Sequence 142091,
15	14.2	71.0	25	55	US-60-234-017-420702	Sequence 420702,
16	14.2	71.0	25	55	US-60-234-017-439150	Sequence 439150,
17	13.8	69.0	25	55	US-60-233-166-188071	Sequence 188071,
18	13.8	69.0	25	55	US-60-233-166-329525	Sequence 329525,
19	13.8	69.0	25	55	US-60-233-166-329641	Sequence 329641,
20	13.8	69.0	25	55	US-60-234-017-22543	Sequence 22543, A
21	13.8	69.0	25	55	US-60-234-017-365211	Sequence 365211,
22	13.6	68.0	25	26	US-09-660-220-54619	Sequence 54619, A
23	13.6	68.0	25	55	US-60-233-166-51615	Sequence 51615, A
24	13.6	68.0	25	55	US-60-233-166-409875	Sequence 409875,
25	13.6	68.0	25	55	US-60-234-017-24188	Sequence 24188, A
26	13.6	68.0	25	55	US-60-234-017-42888	Sequence 42888, A
27	13.6	68.0	25	55	US-60-234-017-57516	Sequence 57516, A
28	13.6	68.0	25	55	US-60-234-017-153880	Sequence 153880,
29	13.6	68.0	25	55	US-60-234-017-523545	Sequence 523545,
30	13.4	67.0	21	3	US-07-918-259-7	Sequence 7, Appl
31	13.4	67.0	25	26	US-09-660-220-71111	Sequence 71111, A
32	13.4	67.0	25	55	US-60-233-166-63810	Sequence 63810, A
33	13.4	67.0	25	55	US-60-233-166-63910	Sequence 63910, A
34	13.2	66.0	25	26	US-09-660-220-11255	Sequence 11255,
35	13.2	66.0	25	26	US-09-660-220-111262	Sequence 111262,
36	13.2	66.0	25	26	US-09-660-220-111262	Sequence 111262,
37	13.2	66.0	25	55	US-60-232-638-101075	Sequence 101075,
38	13.2	66.0	25	55	US-60-233-166-95260	Sequence 95260, A
39	13.2	66.0	25	55	US-60-233-166-201189	Sequence 201189,
40	13.2	66.0	25	55	US-60-233-166-320476	Sequence 320476,
41	13.2	66.0	25	55	US-60-233-166-335443	Sequence 335443,
42	13.2	66.0	25	55	US-60-233-166-397247	Sequence 397247,
43	13.2	66.0	25	55	US-60-233-620-125356	Sequence 125356,
44	13.2	66.0	25	55	US-60-234-017-174077	Sequence 174077,
45	13.2	66.0	25	55	US-60-234-017-215290	Sequence 215290,

ALIGNMENTS

RESULT 1
PCT-US00-18999-11
; Sequence 11, Application PC/TUS0018999
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Monia, Brett P.
; APPLICANT: Gaarde, William A.
; APPLICANT: Nero, Pamela S.
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
; FILE REFERENCE: ISPH-0476
; CURRENT APPLICATION NUMBER: PCT/US00/18999
; PRIOR FILING DATE: 2000-07-13
; PRIOR APPLICATION NUMBER: 09/377,310
; PRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
PCT-US00-18999-11

Query Match 100.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 agtaccagggtgagctcttag 20
|||||
Db 1 agtaccagggtgagctcttag 20

RESULT 2
US-09-377-310-11
; Sequence 11, Application US/09377310A
; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P.
; APPLICANT: Gaarde, William A.
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
; FILE REFERENCE: ISPH-0389
; CURRENT APPLICATION NUMBER: US/09/377,310A
; CURRENT FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
US-09-377-310-11

Query Match 100.0%; Score 20; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 agtaccagggtgagctcttag 20
|||||
Db 1 agtaccagggtgagctcttag 20

RESULT 3
US-09-757-100B-11
; Sequence 11, Application US/09757100B

; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P.
; APPLICANT: Gaarde, William A.
; APPLICANT: Nero, Pamela S.
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
; FILE REFERENCE: ISPH-0533
; CURRENT APPLICATION NUMBER: US/09/757,100B
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 09/377,310
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/US00/18999
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
US-09-757-100B-11

Query Match 100.0%; Score 20; DB 29; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 agtaccagggtgagctcttag 20
|||||
Db 1 agtaccagggtgagctcttag 20

RESULT 4
US-60-233-166-320910/c
; Sequence 320910, Application US/60233166
; GENERAL INFORMATION:
; APPLICANT: Affymetrix, Inc.
; APPLICANT: Mittmann
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat
; FILE REFERENCE: 3112
; CURRENT APPLICATION NUMBER: US/60/233,166
; CURRENT FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 420907
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 320910
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank L08493
US-60-233-166-320910

Query Match 79.0%; Score 15.8; DB 55; Length 25;
Best Local Similarity 89.5%; Pred. No. 5.2e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 gtaccagggtgagctcttag 20
|||
Db 24 GTATCAGGTGAGCTCTTAG 6

RESULT 5
US-60-233-357-9034/c
; Sequence 9034, Application US/602333357
; GENERAL INFORMATION:
; APPLICANT: Affymetrix, Inc.
; APPLICANT: Mittmann
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3114

; CURRENT APPLICATION NUMBER: US/60/233,357
; CURRENT FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 21305
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9034
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank L08493
US-60-233-357-9034

Query Match 79.0%; Score 15.8; DB 55; Length 25;
Best Local Similarity 89.5%; Pred. No. 5.2e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 gtaccacggtagtcttag 20
||| ||||| ||||| |||||

Db 24 GTAATCAGGTGAGTCTTAG 6

RESULT 6

US-60-233-166-329526
; Sequence 329526, Application US/60233166
; GENERAL INFORMATION:
; APPLICANT: Mittmann
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat
; FILE REFERENCE: 3112
; CURRENT APPLICATION NUMBER: US/60/233,166
; CURRENT FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 420907
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 329526
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank M31725
US-60-233-166-329526

Query Match 76.0%; Score 15.2; DB 55; Length 25;
Best Local Similarity 85.0%; Pred. No. 1.1e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 agtaccacggtagtcttag 20
||| ||||| ||||| |||||

Db 3 agaaccacggtaaatcttag 22

RESULT 7

US-60-233-166-329643
; Sequence 329643, Application US/60233166
; GENERAL INFORMATION:
; APPLICANT: Mittmann
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat
; FILE REFERENCE: 3112
; CURRENT APPLICATION NUMBER: US/60/233,166
; CURRENT FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 420907
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 329643
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank M31725
US-60-233-166-329643

Query Match 76.0%; Score 15.2; DB 55; Length 25;
Best Local Similarity 85.0%; Pred. No. 1.1e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 agtaccacggtagtcttag 20
||| ||||| ||||| |||||

Db 6 agaaccacggtaaatcttag 25

RESULT 8

US-60-233-166-329644
; Sequence 329644, Application US/60233166
; GENERAL INFORMATION:
; APPLICANT: Mittmann
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat
; FILE REFERENCE: 3112
; CURRENT APPLICATION NUMBER: US/60/233,166
; CURRENT FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 420907
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 329644
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank M31725
US-60-233-166-329644

Query Match 76.0%; Score 15.2; DB 55; Length 25;
Best Local Similarity 85.0%; Pred. No. 1.1e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 agtaccacggtagtcttag 20
||| ||||| ||||| |||||

Db 5 agaaccacggtaaatcttag 24

RESULT 9

PCT-US00-18999-31
; Sequence 31, Application PC/TUS0018999
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Monia, Brett P.
; APPLICANT: Gaarde, William A.
; APPLICANT: Nero, Pamela S.
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
; FILE REFERENCE: ISPH-0476
; CURRENT APPLICATION NUMBER: PCT/US00/18999
; CURRENT FILING DATE: 2000-07-13
; PRIOR APPLICATION NUMBER: 09/377,310
; PRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 31
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
PCT-US00-18999-31

Query Match 75.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 taccacggtagtctt 17

Db 1 taccacggtagtct 15
|||||

RESULT 10

US-09-377-310-31
; Sequence 31, Application US/09377310A
; GENERAL INFORMATION:
; APPLICANT: Mittmann, M
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of Mus
; FILE REFERENCE: 3115
; CURRENT APPLICATION NUMBER: US/60/234,017
; CURRENT FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 605887
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
US-09-377-310-31

Query Match 75.0%; Score 15; DB 17; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 taccacggtagtct 17
|||||

Db 1 taccacggtagtct 15

RESULT 11

US-09-757-100B-31
; Sequence 31, Application US/09757100B
; GENERAL INFORMATION:
; APPLICANT: Mittmann, M
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of
; FILE REFERENCE: 3116
; CURRENT APPLICATION NUMBER: US/60/233,620
; CURRENT FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 131820
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank AC005724
US-09-757-100B-31

Query Match 75.0%; Score 15; DB 29; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 taccacggtagtct 17
|||||

Db 1 taccacggtagtct 15

RESULT 12

US-60-234-017-22548

; Sequence 22548, Application US/60234017
; GENERAL INFORMATION:
; APPLICANT: Mittmann, M
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of Mus
; FILE REFERENCE: 3115
; CURRENT APPLICATION NUMBER: US/60/234,017
; CURRENT FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 605887
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22548
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank AJ001261
US-60-234-017-22548

Query Match 74.0%; Score 14.8; DB 55; Length 25;
Best Local Similarity 88.9%; Pred. No. 1.8e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 gtaccacggtagtctta 19
|||||

Db 5 gtaaccatgtgagtctta 22

RESULT 13

US-60-233-620-18028
; Sequence 18028, Application US/60233620
; GENERAL INFORMATION:
; APPLICANT: Mittmann, M
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of
; FILE REFERENCE: 3116
; CURRENT APPLICATION NUMBER: US/60/233,620
; CURRENT FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 131820
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18028
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank AC005724
US-60-233-620-18028

Query Match 72.0%; Score 14.4; DB 55; Length 25;
Best Local Similarity 93.8%; Pred. No. 2.9e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 cccacggtagtcttag 20
|||||

Db 10 cccacgtgagtcttag 25

RESULT 14

US-60-234-017-142091
; Sequence 142091, Application US/60234017
; GENERAL INFORMATION:
; APPLICANT: Mittmann, M
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of Mus
; FILE REFERENCE: 3115
; CURRENT APPLICATION NUMBER: US/60/234,017
; CURRENT FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 605887
; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 142091
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank AF591702
; US-60-234-017-142091

Query Match 71.0%; Score 14.2; DB 55; Length 25;
Best Local Similarity 84.2%; Pred. No. 3.7e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 gtaccaggtagtcttag 20
||| ||||| ||||| ||
Db 4 gtaccaggtaagtctgag 22

RESULT 15
US-60-234-017-420702
; Sequence 420702, Application US/60234017
; GENERAL INFORMATION:
; APPLICANT: Mittmann, M
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of Mus
; TITLE OF INVENTION: musculus
; FILE REFERENCE: 3115
; CURRENT APPLICATION NUMBER: US/60/234,017
; NUMBER OF SEQ ID NOS: 605887
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 420702
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank AU024707
; US-60-234-017-420702

Query Match 71.0%; Score 14.2; DB 55; Length 25;
Best Local Similarity 84.2%; Pred. No. 3.7e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 agtaccaggtagtcttta 19
||| ||||| ||||| ||
Db 1 agtccccaagtgtgtcttta 19

Search completed: October 2, 2001, 21:50:14
Job time: 24527 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: October 2, 2001, 16:55:02 ; Search time 2173.58 Seconds
(without alignments)
19.290 Million cell updates/sec

Title: US-09-757-100B-11

Perfect score: 20

Sequence: 1 agtaccagggtgagcttag 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1895189 seqs, 1048201267 residues

Total number of hits satisfying chosen parameters: 299022

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending_Patents_NA_New.*

- 1: /cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq.*
- 2: /cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq.*
- 3: /cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq.*
- 4: /cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq.*
- 5: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq.*
- 6: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq1.*
- 7: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq2.*
- 8: /cgn2_6/ptodata/2/pna/US60_NEW_COMB.seq.*

pred, No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
c 1	12.8	64.0	25	6	US-09-857-581-65
2	12.4	62.0	33	7	US-09-672-217-122
3	12.4	62.0	33	7	US-09-672-217-223
4	12	60.0	22	1	PCT-US00-00358-16
5	12	60.0	25	6	US-09-866-108-4143
6	12	60.0	25	6	US-09-866-108-4144
7	12	60.0	25	6	US-09-866-108-4145
8	12	60.0	25	6	US-09-866-108-4146
9	12	60.0	25	6	US-09-866-108-4147
10	12	60.0	25	6	US-09-866-108-4148
11	12	60.0	44	8	US-60-252-833-24181
12	11.8	59.0	17	6	US-09-546-745A-4802
13	11.6	58.0	29	7	US-09-724-671-10607
14	11.6	58.0	48	8	US-60-253-457-42408
15	11.4	57.0	26	6	US-09-863-806-69
16	11.4	57.0	31	6	US-09-801-274-1705
17	11.2	56.0	17	6	US-09-522-240A-30
18	11.2	56.0	17	6	US-09-866-108-7712
19	11.2	56.0	17	6	US-09-866-108-7713
20	11.2	56.0	17	6	US-09-513-063-18
21	11.2	56.0	17	6	US-09-817-879-2232
22	11.2	56.0	17	6	US-09-817-879-2233
23	11.2	56.0	20	6	US-09-895-007-115
24	11.2	56.0	20	7	US-09-920-313-115
25	11.2	56.0	20	7	US-09-659-845A-82

C	26	11.2	56.0	20	7	US-09-899-440-1	Sequence 1, Appl
27	11.2	56.0	22	7	US-09-848-103B-51	Sequence 51, Appl	
28	11.2	56.0	25	6	US-09-866-108-12604	Sequence 12604, A	
29	11.2	56.0	25	6	US-09-866-108-12605	Sequence 12605, A	
30	11.2	56.0	25	6	US-09-866-108-12606	Sequence 12606, A	
31	11.2	56.0	25	6	US-09-866-108-12607	Sequence 12607, A	
32	11.2	56.0	25	6	US-09-866-108-12608	Sequence 12608, A	
33	11.2	56.0	25	6	US-09-866-108-12609	Sequence 12609, A	
34	11.2	56.0	25	6	US-09-866-108-12610	Sequence 12610, A	
35	11.2	56.0	25	6	US-09-866-108-12611	Sequence 12611, A	
36	11.2	56.0	25	6	US-09-866-108-12612	Sequence 12612, A	
37	11.2	56.0	25	6	US-09-866-108-12613	Sequence 12613, A	
38	11.2	56.0	25	7	US-09-848-103B-49	Sequence 49, Appl	
39	11.2	56.0	36	5	US-09-274-553C-2830	Sequence 2830, Ap	
40	11.2	56.0	38	7	US-09-864-785-1301	Sequence 1301, Ap	
41	11.2	56.0	50	5	US-09-699-011A-308	Sequence 308, App	
42	11	55.0	25	5	US-09-930-803-7	Sequence 7, Appl	
43	11	55.0	25	6	US-09-866-108-4142	Sequence 4142, Ap	
44	11	55.0	25	6	US-09-866-108-4149	Sequence 4149, Ap	
45	11	55.0	25	6	US-09-866-108-4254	Sequence 4254, Ap	

ALIGNMENTS

RESULT 1
US-09-857-581-65/c
; Sequence 65, Application US/09857581
; GENERAL INFORMATION:
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
; FILE REFERENCE: Bbl339 PCT
; CURRENT APPLICATION NUMBER: US/09/857,581
; CURRENT FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: 60/117,769
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: 60/144,783
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/156,094
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 65
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:PCR PRIMER
US-09-857-581-65

Query Match 64.0%; Score 12.8; DB 6; Length 25;
Best Local Similarity 87.5%; Pred. No. 2.1e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 cccagggtgagcttag 20
|||||
Db 17 CCCAGGTGAGTTTCAG 2

RESULT 2
US-09-672-217-122
; Sequence 122, Application US/09672217
; GENERAL INFORMATION:
; APPLICANT: DIAZ, MARK
; APPLICANT: FELL, JACK
; TITLE OF INVENTION: METHOD OF IDENTIFYING PATHOGENIC CRYPTOCOCCI
; FILE REFERENCE: 086222/0143
; CURRENT APPLICATION NUMBER: US/09/672,217
; CURRENT FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/156,598
; PRIOR FILING DATE: 1999-09-29

; NUMBER OF SEQ ID NOS: 301
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 122
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer/Probe
US-09-672-217-122

Query Match 62.0%; Score 12.4; DB 7; Length 33;
Best Local Similarity 92.9%; Pred. No. 3.7e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 acccaggtgagtct 17
||| ||||| ||||| ||
Db 17 acccaggtgagtat 30

RESULT 3
US-09-672-217-223
; Sequence 223, Application US/09672217
; GENERAL INFORMATION:
; APPLICANT: FELL, JACK
; APPLICANT: DIAZ, MARA
; TITLE OF INVENTION: METHOD OF IDENTIFYING PATHOGENIC CRYPTOCOCCI
; CURRENT APPLICATION NUMBER: US/09/672,217
; CURRENT FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/156,598
; PRIOR FILING DATE: 1999-09-29
; NUMBER OF SEQ ID NOS: 301
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 223
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer/Probe
US-09-672-217-223

Query Match 62.0%; Score 12.4; DB 7; Length 33;
Best Local Similarity 92.9%; Pred. No. 3.7e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 acccaggtgagtct 17
||| ||||| ||||| ||
Db 17 acccaggtgagtat 30

RESULT 4
PCT-US00-00358-16
; Sequence 16, Application PC/TUS0000358
; GENERAL INFORMATION:
; APPLICANT: pecker, iris
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ENCODED THEREBY DISTANTLY HOMOLOG
; FILE REFERENCE: 00/20105
; CURRENT APPLICATION NUMBER: PCT/US00/00358
; CURRENT FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: 60/140,801
; PRIOR FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 16
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Synthetic Oligonucleotide
PCT-US00-00358-16

Query Match 60.0%; Score 12; DB 1; Length 22;
Best Local Similarity 75.0%; Pred. No. 5.7e+03;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 agtaccacaggtgagtccttag 20
||| ||||| ||||| ||
Db 2 agcagccaggtgagcccaag 21

RESULT 5
US-09-866-108-4143
; Sequence 4143, Application US/09866108
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 4143
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-4143

Query Match 60.0%; Score 12; DB 6; Length 25;
Best Local Similarity 75.0%; Pred. No. 5.9e+03;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 agtaccacaggtgagtccttag 20
||| ||||| ||||| ||
Db 6 agaagacaggtgagcctcag 25

```

; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: A6MICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: A6MICA Sequence Listing Engine
; SEQ ID NO 4145
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-4145

Query Match 60.0%; Score 12; DB 6; Length 25;
Best Local Similarity 75.0%; Pred. No. 5.9e+03;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 agtaccagggtgagtccttag 20
   ||| ||||| |||
Db 4 agaagacaggtagcctcag 23

RESULT 8
US-09-866-108-4146
; Sequence 4146, Application US/09866108
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: A6MICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359

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RESULT          9
US-09-866-108-4147
; Sequence 4147, Application US/09866108
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYO5IN-LIKE GENE EXPRES
; FILE REFERENCE: AEMCMA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665

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RESULT 10
US-09-866-108-4148
Sequence 4148, Application US/09866108
GENERAL INFORMATION:
APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AEOICA-7
CURRENT APPLICATION NUMBER: US/09/866.108
CURRENT FILING DATE: 2001-05-25
PRIORITY APPLICATION NUMBER: US 60/207,456
PRIORITY FILING DATE: 2000-05-26
PRIORITY APPLICATION NUMBER: GB 24263.6
PRIORITY FILING DATE: 2000-10-04
PRIORITY APPLICATION NUMBER: US 60/236,359
PRIORITY FILING DATE: 2000-09-27
PRIORITY APPLICATION NUMBER: PCT/US01/006666
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/006657
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/006664
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/006669
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/006665
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/006668
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/006663
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/006662
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/006661
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/006670

; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Acomica Sequence Listing Engine
; SEQ ID NO 4148
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-4148

Query Match 60.0%; Score 12; DB 6; Length 25;
Best Local Similarity 75.0%; Pred. No. 5.9e+03;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 agtaccagggtgagctcttag 20
||| ||||| |||
Db 1 agaagacagggtgagcctcag 20

RESULT 11
US-60-252-833-24181/c
; Sequence 24181, Application US/60252833
; GENERAL INFORMATION:
; APPLICANT: Glenn, Matthew
; TITLE OF INVENTION: Compositions isolated from bovine
; TITLE OF INVENTION: tissues and methods for their use.
; FILE REFERENCE: 1052P2
; CURRENT APPLICATION NUMBER: US/60/252,833
; CURRENT FILING DATE: 2000-11-21
; NUMBER OF SEQ ID NOS: 43535
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24181
; LENGTH: 44
; TYPE: DNA
; ORGANISM: Bovine
US-60-252-833-24181

Query Match 60.0%; Score 12; DB 8; Length 44;
Best Local Similarity 75.0%; Pred. No. 6.4e+03;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 agtaccagggtgagctcttag 20
||| ||||| |||
Db 21 AGTACTCAGGAGGAGCTTTAG 2

RESULT 12
US-09-546-745A-4802/c
; Sequence 4802, Application US/09546745A
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: Zwick, Michael
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Regulation of Repressor Genes using Nucleic Acid Molecules
; FILE REFERENCE: 237/193
; CURRENT APPLICATION NUMBER: US/09/546,745A
; CURRENT FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 7043
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4802
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid

US-09-546-745A-4802

Query Match 59.0%; Score 11.8; DB 6; Length 17;
Best Local Similarity 86.7%; Pred. No. 7.1e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 ccagggtgagctcttag 20
||| ||||| |||
Db 15 CCAGGTGAGGCGTAG 1

RESULT 13
US-09-724-671-10607/c
; Sequence 10607, Application US/09724671
; GENERAL INFORMATION:
; APPLICANT: Watson, James D
; APPLICANT: Murison, James G
; TITLE OF INVENTION: Polynucleotides, polypeptides expressed
; TITLE OF INVENTION: by the polynucleotides and methods for their use.
; FILE REFERENCE: 1050U2
; CURRENT APPLICATION NUMBER: US/09/724,671
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: U.S. No. 60/171,678
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 21907
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10607
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Mouse
US-09-724-671-10607

Query Match 58.0%; Score 11.6; DB 7; Length 29;
Best Local Similarity 77.8%; Pred. No. 1e+04;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 agtaccagggtgagctctt 18
||| ||||| |||
Db 22 AGTGCCAGGTGAGTGTT 5

RESULT 14
US-60-253-457-42408
; Sequence 42408, Application US/60253457
; GENERAL INFORMATION:
; APPLICANT: Havukkala, Ilkka J
; TITLE OF INVENTION: Polynucleotides, isolated from plants
; TITLE OF INVENTION: and methods for their use.
; FILE REFERENCE: 1054P2
; CURRENT APPLICATION NUMBER: US/60/253,457
; CURRENT FILING DATE: 2000-11-27
; NUMBER OF SEQ ID NOS: 48893
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 42408
; LENGTH: 48
; TYPE: DNA
; ORGANISM: Pinus radiata
US-60-253-457-42408

Query Match 58.0%; Score 11.6; DB 8; Length 48;
Best Local Similarity 77.8%; Pred. No. 1.1e+04;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 taccagggtgagctcttag 20
||| ||||| |||
Db 9 tacgagggtgagattcag 26

RESULT 15
US-09-863-806-69/c

Sequence 69, Application US/09863806
GENERAL INFORMATION:
APPLICANT: Sidransky, David
TITLE OF INVENTION: DETECTION OF NEOPLASIM BY ANALYSIS OF SALIVA
NUMBER OF SEQUENCES: 195
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/863,806
FILING DATE: 22-May-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/038,637
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/152,313
FILING DATE: 12-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/146001
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 69:
US-09-863-806-69

Query Match 57.0%; Score 11.4; DB 6; Length 26;
Best Local Similarity 92.3%; Pred. NO. 1.3e+04;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 7 caggtagagtcctta 19
||| |||||
DB 23 CAAGTGAGTCTTA 11

Search completed: October 2, 2001, 16:55:02
Job time: 17665 sec

09/757,100